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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:24:27 ; Search time 16 Seconds
(without alignments)
12.906 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 11020

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCUOS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	25	100.0	4	1 US-07-934-553-5	Sequence 5, Appli
2	25	100.0	4	1 US-07-932-200-6	Sequence 6, Appli
3	25	100.0	4	1 US-08-022-381A-1	Sequence 1, Appli
4	25	100.0	4	1 US-08-225-474-5	Sequence 5, Appli
5	25	100.0	4	1 US-08-365-759-2	Sequence 2, Appli
6	25	100.0	4	1 US-08-475-827A-1	Sequence 1, Appli
7	25	100.0	4	2 US-08-387-749-6	Sequence 6, Appli
8	25	100.0	4	2 US-08-747-137-81	Sequence 81, Appli
9	25	100.0	4	2 US-08-753-781-2	Sequence 2, Appli
10	25	100.0	4	3 US-08-993-165-6	Sequence 6, Appli
11	25	100.0	4	3 US-08-611-395-5	Sequence 5, Appli
12	25	100.0	4	4 US-09-540-448-6	Sequence 6, Appli
13	25	100.0	4	4 US-09-243-640-4	Sequence 4, Appli
14	25	100.0	4	4 US-08-929-847-6	Sequence 6, Appli
15	25	100.0	4	5 PCT-US93-08251-6	Sequence 6, Appli
16	25	100.0	4	5 PCT-US95-07542-4	Sequence 4, Appli
17	19	76.0	4	1 US-07-917-034A-6	Sequence 6, Appli
18	19	76.0	4	1 US-07-917-034A-12	Sequence 12, Appli
19	19	76.0	4	4 US-09-086-168B-1	Sequence 1, Appli
20	19	76.0	4	6 5425936-4	Patent No. 5425936
21	19	76.0	4	6 5425936-8	Patent No. 5425936
22	19	76.0	4	6 5433940-1	Patent No. 5433940
23	18	72.0	3	1 US-07-816-679A-9	Sequence 9, Appli
24	18	72.0	3	1 US-08-365-759-1	Sequence 1, Appli
25	18	72.0	3	1 US-08-213-897A-12	Sequence 12, Appli
26	18	72.0	3	2 US-08-476-014-8	Sequence 8, Appli
27	18	72.0	3	5 PCT-US92-11270-9	Sequence 9, Appli

28	18	72.0	4	1 US-07-932-200-7	Sequence 7, Appli
29	18	72.0	4	1 US-07-932-200-8	Sequence 8, Appli
30	18	72.0	4	1 US-07-932-200-9	Sequence 9, Appli
31	18	72.0	4	1 US-07-776-257-1	Sequence 1, Appli
32	18	72.0	4	1 US-07-776-257-2	Sequence 2, Appli
33	18	72.0	4	1 US-08-127-351-50	Sequence 50, Appli
34	18	72.0	4	1 US-08-095-162-9	Sequence 9, Appli
35	18	72.0	4	1 US-08-365-759-4	Sequence 4, Appli
36	18	72.0	4	1 US-08-480-367B-50	Sequence 50, Appli
37	18	72.0	4	1 US-08-487-221A-50	Sequence 50, Appli
38	18	72.0	4	1 US-08-480-370-50	Sequence 50, Appli
39	18	72.0	4	1 US-08-294-434-4	Sequence 4, Appli
40	18	72.0	4	1 US-08-284-434-11	Sequence 11, Appli
41	18	72.0	4	1 US-08-457-166-4	Sequence 4, Appli
42	18	72.0	4	1 US-08-457-166-11	Sequence 11, Appli
43	18	72.0	4	1 US-08-299-636-30	Sequence 30, Appli
44	18	72.0	4	1 US-08-279-155-30	Sequence 30, Appli
45	18	72.0	4	1 US-08-464-456-28	Sequence 28, Appli
46	18	72.0	4	1 US-08-470-220A-9	Sequence 9, Appli
47	18	72.0	4	1 US-08-703-988A-30	Sequence 30, Appli
48	18	72.0	4	1 US-08-463-052-28	Sequence 28, Appli
49	18	72.0	4	2 US-08-480-551-28	Sequence 28, Appli
50	18	72.0	4	2 US-08-387-749-7	Sequence 7, Appli
51	18	72.0	4	2 US-08-387-749-8	Sequence 8, Appli
52	18	72.0	4	2 US-08-387-749-9	Sequence 9, Appli
53	18	72.0	4	2 US-08-922-267A-75	Sequence 75, Appli
54	18	72.0	4	2 US-08-685-589A-35	Sequence 35, Appli
55	18	72.0	4	2 US-08-685-589A-36	Sequence 36, Appli
56	18	72.0	4	2 US-08-612-842-30	Sequence 30, Appli
57	18	72.0	4	3 US-08-967-374-9	Sequence 9, Appli
58	18	72.0	4	3 US-08-927-128-10	Sequence 10, Appli
59	18	72.0	4	3 US-09-219-849-14	Sequence 14, Appli
60	18	72.0	4	3 US-08-960-054A-30	Sequence 30, Appli
61	18	72.0	4	3 US-08-958-993A-30	Sequence 30, Appli
62	18	72.0	4	4 US-08-959-208A-26	Sequence 26, Appli
63	18	72.0	4	4 US-09-505-991-9	Sequence 9, Appli
64	18	72.0	4	4 US-08-278-774-5	Sequence 5, Appli
65	18	72.0	4	4 US-09-925-715-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
US-07-934-553-5
; Sequence 5, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING Ige
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGWIS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:

NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-5

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 2
US-07-932-200-6
Sequence 6, Application US/07932200
Patent No. 536862
GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: LE BRETON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FILING DATE: 21-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON=1B
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-932-200-6

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

Db 1 GPRP 4
RESULT 3
US-08-022-381A-1
Sequence 1, Application US/08022381A
Patent No. 5478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-022-381A-1

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 4
US-08-225-474-5
Sequence 5, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: Ige Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

US-08-022-381A-1
Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

US-08-022-381A-1
Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

US-08-022-381A-1
Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

US-08-022-381A-1
Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

US-08-022-381A-1
Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STREET: 100 S. Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/225,474
FILING DATE: 21-AUG-1992
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8900
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-225-474-5

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 5
US-08-365-759-2
Sequence 2, Application US/08/365759
Patent No. 5563041
GENERAL INFORMATION:
APPLICANT: Reers, Martin
TITLE OF INVENTION: Method for Determining Platelet
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Toohay, Kimberlin M.

REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 05552.1378-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-365-759-2

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 6
US-08-475-827A-1
Sequence 1, Application US/08/475827A
Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
TITLE OF INVENTION: Peptide Amides, Processes For the
Preparation Thereof And Agents Containing These As
Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Lori-Ann
REGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 05552.1054-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-08-475-827A-1
Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 7
US-08-387-749-6
; Sequence 6, Application US/08387749
; Patent No. 5814460
; GENERAL INFORMATION:
; APPLICANT: VENTON, DUANE L.
; APPLICANT: HOPFINGER, ANTON J.
; APPLICANT: LE BRITON, GUY
; TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
; TITLE OF INVENTION: USEFUL PEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,749
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08231
; FILING DATE: 09-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/932,200
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,315
; FILING DATE: 21-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00891
; FILING DATE: 14-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/480,865
; FILING DATE: 14-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: VENTON-1C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-387-749-6
Query Match 100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

Query Match 100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

US-08-747-137-81
; Sequence 81, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
US-08-747-137-81
Query Match 100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 9
US-08-753-781-2
; Sequence 2, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
```


APPLICANT: Bush, Larry R.
APPLICANT: Swenson, Stephen
APPLICANT: Flores Sanchez, Eladio
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
FILE REFERENCE: DIII 124
CURRENT APPLICATION NUMBER: US/08/753,781C
CURRENT FILING DATE: 1996-12-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-08-753-781-2

Query Match 100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 10
US-08-993-165-6
Sequence 6, Application US/08993165A
Patent No. 6123923
GENERAL INFORMATION:
APPLICANT: Unger, Evan C
APPLICANT: Wu, Yungui
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6123923a1 Sequence
US-08-993-165-6

Query Match 100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 11
US-08-611-395-5
Sequence 5, Application US/08611395
Patent No. 6168939
GENERAL INFORMATION:
APPLICANT: SASAKI, MASAHITO
BOSMAN, BOUKJE
TAN, PARIS S. T.
TAKAFUJI, SHIN'ICHI
IWASAKI, TAISUKE
TITLE OF INVENTION: NOVEL ENDOPEPTIDASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,395
FILING DATE: 06-Mar-1996
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-611-395-5

Query Match 100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 12
US-09-540-448-6
Sequence 6, Application US/09540448
Patent No. 6403056
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TITLE OF INVENTION: Charged Lipids and Uses For The Same
FILE REFERENCE: UNGR1592
CURRENT APPLICATION NUMBER: US/09/540,448
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 08/925,353
PRIOR FILING DATE: 1997-09-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
US-09-540-448-6

Query Match 100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 13
US-09-243-640-4
Sequence 4, Application US/09243640
Patent No. 6521211

GENERAL INFORMATION:
APPLICANT: Unger, Evan C
TITLE OF INVENTION: Methods of Imaging And Treatment With Targeted Compositions
FILE REFERENCE: DUP-0463
CURRENT APPLICATION NUMBER: US/09/243,640
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 08/660,032
PRIOR FILING DATE: 1996-06-06
PRIOR APPLICATION NUMBER: 08/640,464
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/497,684
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/218,660
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/073,913
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
US-09-243-640-4

Query Match 100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 14
US-08-929-847-6
Sequence 6, Application US/08929847
Patent No. 6548047
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
FILE REFERENCE: BMS0441
CURRENT APPLICATION NUMBER: US/08/929,847
CURRENT FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-6

Query Match 100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 15
PCT-US93-08231-6
Sequence 6, Application PC/TUS9308231
GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.

APPLICANT: LE BRETON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08231
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTONIC.PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08231-6

Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 16
PCT-US95-07542-4
Sequence 4, Application PC/TUS9507542
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF TRANSMEMBRANE RECEPTORS
NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07542
FILING DATE: 13-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/260,514
FILING DATE: 15-JUN-1994
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal

ORIGINAL SOURCE:
ORGANISM: Ligand sequence recognized by integrin
PCT-US95-07542-4

Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 17
US-07-917-034A-6
; Sequence 6, Application US/07917034A
; Patent No. 5427927
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher,
; APPLICANT: G nter, Dony, Carola
; TITLE OF INVENTION: Process For The Enzymatic Cleavage
; TITLE OF INVENTION: of Recombinant Proteins Using IGA Proteases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/917,034A
; FILING DATE: 19920830
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 1-Feb-1991
; PRIOR APPLICATION NUMBER: DE 40 39 415.8
; FILING DATE: 10-Dec-1990
; APPLICATION NUMBER: DE 40 15 922.1
; FILING DATE: 17-May-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 15 921.3
; FILING DATE: 17-May-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 03 149.7
; FILING DATE: 3-Feb-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5427927man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: HUBR 1018
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-917-034A-6

Query Match 76.0%; Score 19; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
Db 2 PRP 4

RESULT 18
US-07-917-034A-12
; Sequence 12, Application US/07917034A
; Patent No. 5427927
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher,
; APPLICANT: G nter, Dony, Carola
; TITLE OF INVENTION: Process For The Enzymatic Cleavage
; TITLE OF INVENTION: of Recombinant Proteins Using IGA Proteases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/917,034A
; FILING DATE: 19920830
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 1-Feb-1991
; PRIOR APPLICATION NUMBER: DE 40 15 922.1
; FILING DATE: 17-May-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 15 921.3
; FILING DATE: 17-May-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 03 149.7
; FILING DATE: 3-Feb-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5427927man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: HUBR 1018
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-917-034A-12

Query Match 76.0%; Score 19; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
Db 1 PRP 3

RESULT 19
US-09-086-1688-1
; Sequence 1, Application US/090861688
; Patent No. 6638941
; GENERAL INFORMATION:
; APPLICANT: Castelhamo, Arlindo
; APPLICANT: Witter, David
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED PEPTIDOMIMETICS AS BETA-TURN
; TITLE OF INVENTION: TEMPLATES AND MODULATORS OF SH3 DOMAINS

```
; FILE REFERENCE: 60384-B
; CURRENT APPLICATION NUMBER: US/09/086,168B
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SH3 test peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(4)
; OTHER INFORMATION: Synthetic Peptide
US-09-086-168B-1

Query Match          76.0%; Score 19; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PRP 4
Db      1 PRP 3

RESULT 20
;Patent No. 5425936
;APPLICANT: MARAGANORE, JOHN M.; JABLONSKI, JO-ANN M.; BOURDON,
;PAUL R.
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,549
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 652,929
; FILING DATE: 08-FEB-1991
; APPLICATION NUMBER: 549,388
; FILING DATE: 06-JUL-1990
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
;SEQ ID NO:4
; LENGTH: 4
5425936-4

Query Match          76.0%; Score 19; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PRP 4
Db      2 PRP 4

RESULT 21
;Patent No. 5425936
;APPLICANT: MARAGANORE, JOHN M.; JABLONSKI, JO-ANN M.; BOURDON,
;PAUL R.
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,549
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 652,929
; FILING DATE: 08-FEB-1991
; APPLICATION NUMBER: 549,388
; FILING DATE: 06-JUL-1990
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
;SEQ ID NO:4
; LENGTH: 4
5425936-4

Query Match          76.0%; Score 19; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PRP 4
Db      2 PRP 4

RESULT 22
;Patent No. 5433940
;APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,259
; FILING DATE: 17-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 548,388
; FILING DATE: 06-JUL-1989
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
;SEQ ID NO:1
; LENGTH: 4
5433940-1

Query Match          76.0%; Score 19; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PRP 4
Db      2 PRP 4

RESULT 23
US-07-816-679A-9
; Sequence 9, Application US/07816679A
; Patent No. 5298599
; GENERAL INFORMATION:
; APPLICANT: Rezaie, Alireza
; APPLICANT: Esmen, Charles T.
; TITLE OF INVENTION: Expression and Purification of
; TITLE OF INVENTION: Recombinant Soluble Tissue Factor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 100 Peachtree Street, Suite 3200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303
; COMEUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,679A
; FILING DATE: 19920103
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730040
; FILING DATE: 12-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/292447
; FILING DATE: 30-DEC-1988
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/583682
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRFL30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-572-6508
; TELEFAX: 404-572-6555
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 1-3
; OTHER INFORMATION: /note= "Thrombin Cleavage Site"
; US-07-816-679A-9

Query Match 72.0%; Score 18; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 24
US-08-365-759-1
; Sequence 1, Application US/08365759
; Patent No. 5563041
; GENERAL INFORMATION:
; APPLICANT: Reers, Martin
; TITLE OF INVENTION: Method for Determining Platelet
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/365,759
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Toohy, Kimberlin M.
; REGISTRATION NUMBER: 35,391
; REFERENCE/DOCKET NUMBER: 05552.1378-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; US-08-365-759-1

Query Match 72.0%; Score 18; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 25
US-08-213-897A-12
; Sequence 12, Application US/08213897A
; Patent No. 5618790
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Protease Mediated Drug Delivery System
; NUMBER OF SEQUENCES: 18
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,897A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/593,867
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/833,183
; FILING DATE: 10-FEB-1992
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-213-897A-12

Query Match 72.0%; Score 18; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 26
US-08-476-014-8
; Sequence 8, Application US/08476014
; Patent No. 5871724
; GENERAL INFORMATION:
; APPLICANT: Iwata, Kenneth K
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Ten Dijke, Peter
; APPLICANT: Haley, John D
; TITLE OF INVENTION: TISSUE-DERIVED TUMOR GROWTH
; TITLE OF INVENTION: INHIBITORS, PREPARATION AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,014
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 22669HZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-014-8

Query Match 72.0%; Score 18; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 27
PCT-US92-11270-9
Sequence 9, Application PC/TUS9211270
GENERAL INFORMATION:
APPLICANT: Rezaie, Alireza
APPLICANT: Esmon, Charles T.
APPLICANT: Morrissey, James H.
TITLE OF INVENTION: Expression and Purification of
TITLE OF INVENTION: Recombinant Soluble Tissue Factor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11270
FILING DATE: 19921229
CLASSIFICATION:
PRIOR APPLICATION DATA: US 07/816679
APPLICATION NUMBER: US 07/816679
FILING DATE: 03-JAN-1992
PRIOR APPLICATION DATA: US 07/730040
APPLICATION NUMBER: US 07/730040
FILING DATE: 12-JUL-1991
PRIOR APPLICATION DATA: US 07/292447
APPLICATION NUMBER: US 07/292447
FILING DATE: 30-DEC-1988
PRIOR APPLICATION DATA: US 07/693682
APPLICATION NUMBER: US 07/693682
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRP130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 1.13
OTHER INFORMATION: /note= "Thrombin Cleavage Site"
PCT-US92-11270-9

Query Match 72.0%; Score 18; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 28
US-07-932-200-7
Sequence 7, Application US/07932200
Patent No. 536862
GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: LE BRETON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FILING DATE: 21-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-932-200-7

Query Match 72.0%; Score 18; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPR 3
Db 1 GPR 3

RESULT 29
US-07-932-200-8
; Sequence 8, Application US/07932200
; Patent No. 5366862
; GENERAL INFORMATION:
; APPLICANT: VENTON, DUANE L.
; APPLICANT: HOPFINGER, ANTON J.
; APPLICANT: LE BRETON, GUY
; TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
; USEFUL PEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/932,200
; FILING DATE: 21-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: VENTON=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-932-200-8

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 30
US-07-932-200-9
; Sequence 9, Application US/07932200
; Patent No. 5366862
; GENERAL INFORMATION:
; APPLICANT: VENTON, DUANE L.
; APPLICANT: HOPFINGER, ANTON J.
; APPLICANT: LE BRETON, GUY
; TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
; USEFUL PEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FILING DATE: 21-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-932-200-9

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 31
US-07-776-257-1
; Sequence 1, Application US/07776257
; Patent No. 5449612
; GENERAL INFORMATION:
; APPLICANT: Lepargneur, Jean-Pierre
; APPLICANT: Contant spouse Pussard,
; APPLICANT: Genevieve
; APPLICANT: Martinoli, Jean-Luc
; APPLICANT: Quentin, Gerard
; TITLE OF INVENTION: Process for identifying Candida by
; means of Chromogenic Substances
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price Holman & Stern
; STREET: 400 Seventh Street N.W.
; CITY: Washington D.C.
; COUNTRY: USA
; ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/776,257
FILING DATE: 19911119
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00233
FILING DATE: 23-MAR-1990
ATTORNEY/AGENT INFORMATION:

QY 1 GPR 3
Db 1 GPR 3

RESULT 30
US-07-932-200-9
; Sequence 9, Application US/07932200
; Patent No. 5366862
; GENERAL INFORMATION:
; APPLICANT: VENTON, DUANE L.
; APPLICANT: HOPFINGER, ANTON J.
; APPLICANT: LE BRETON, GUY
; TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
; USEFUL PEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

NAME: Holman, John C
REGISTRATION NUMBER: 22679
REFERENCE/DOCKET NUMBER: 5885/P-5449NA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-776-257-1

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 2 GPR 4

RESULT 32

US-07-776-257-2
Sequence 2, Application US/07776257
Patent No. 549612
GENERAL INFORMATION:
APPLICANT: Lepargneur, Jean-Pierre
APPLICANT: Contant spouse Pussard,
APPLICANT: Genevieve
APPLICANT: Martinoli, Jean-Luc
APPLICANT: Quantin, Gerard
TITLE OF INVENTION: Process for identifying Candida by
TITLE OF INVENTION: means of Chromogenic Substances
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price Holman & Stern
STREET: 400 Seventh Street N.W.
CITY: Washington D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/776,257
FILING DATE: 19911119
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00233
FILING DATE: 23-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Holman, John C
REGISTRATION NUMBER: 22679
REFERENCE/DOCKET NUMBER: 5885/P-5449NA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-776-257-2

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 2 GPR 4

RESULT 33

US-08-127-351-50
Sequence 50, Application US/08127351
Patent No. 5493761
GENERAL INFORMATION:
APPLICANT: BELINKA JR, BENJAMIN A.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: ALVAREZ, VERNON L.
APPLICANT: WOOD, RICHARD
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
TITLE OF INVENTION: CONSTRUCTS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,351
FILING DATE: 28-SEP-1993
CLASSIFICATION: 534
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-127-351-50

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 1 GPR 3

RESULT 34

US-08-095-162-9
Sequence 9, Application US/08095162
Patent No. 5512459
GENERAL INFORMATION:
APPLICANT: Wagner, Fred W.
APPLICANT: Stout, Jay
APPLICANT: Henriksen, Dennis
APPLICANT: Partridge, Bruce
APPLICANT: Manning, Shane
TITLE OF INVENTION: Enzymatic Method for Modification of
TITLE OF INVENTION: Recombinant Polypeptides
NUMBER OF SEQUENCES: 26

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5512459west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095.162
; FILING DATE: 20-JUL-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,659
; REFERENCE/DOCKET NUMBER: 8648.32-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-095-162-9

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 2 GPR 4

RESULT 35
US-08-365-759-4
; Sequence 4, Application US/08365759
; Patent No. 5563041
; GENERAL INFORMATION:
; APPLICANT: Reers, Martin
; TITLE OF INVENTION: Method for Determining Platelet
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365.759
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Toohay, Kimberlin M.
; REGISTRATION NUMBER: 35,391
; REFERENCE/DOCKET NUMBER: 05552.1378-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa is sarcosine."
; US-08-365-759-4

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 1 GPR 3

RESULT 36
US-08-480-367B-50
; Sequence 50, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA Jr, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-367B-50

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 1 GPR 3

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RESULT 37
US-08-487-221A-50
; Sequence 50, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-487-221A-50

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 1 GPR 3

RESULT 38
US-08-480-370-50
; Sequence 50, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
```

```
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-370-50

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 1 GPR 3

RESULT 39
US-08-294-434-4
; Sequence 4, Application US/08294434
; Patent No. 5635371
; GENERAL INFORMATION:
; APPLICANT: Stout, Jay
; APPLICANT: Wagner, Fred W.
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
; TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
; TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
; TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5635371west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,434
; FILING DATE:
```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 8648.29-US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-294-434-4

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPR 3
Db 2 GPR 4

RESULT 41
US-08-457-166-4
Sequence 4, Application US/08457166
Patent No. 5656456
GENERAL INFORMATION:
APPLICANT: Stout, Jay
APPLICANT: Wagner, Fred W.
APPLICANT: Coolidge, Thomas R.
APPLICANT: Holmquist, Barton
TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
OPERATING SYSTEM: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5656456west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,166
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/091,751
FILING DATE:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 8648.35-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-457-166-4

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPR 3
Db 2 GPR 4

RESULT 40
US-08-294-434-11
Sequence 11, Application US/08294434
Patent No. 5635371
GENERAL INFORMATION:
APPLICANT: Stout, Jay
APPLICANT: Wagner, Fred W.
APPLICANT: Coolidge, Thomas R.
APPLICANT: Holmquist, Barton
TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
OPERATING SYSTEM: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5635371west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,434
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 8648.29-US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPR 3
Db 2 GPR 4

US-08-457-166-4
Sequence 4, Application US/08457166
Patent No. 5656456
GENERAL INFORMATION:
APPLICANT: Stout, Jay
APPLICANT: Wagner, Fred W.
APPLICANT: Coolidge, Thomas R.
APPLICANT: Holmquist, Barton
TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
OPERATING SYSTEM: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5656456west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,166
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/091,751
FILING DATE:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 8648.35-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-457-166-4

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPR 3
Db 2 GPR 4

US-08-457-166-4
Sequence 4, Application US/08457166
Patent No. 5656456
GENERAL INFORMATION:
APPLICANT: Stout, Jay
APPLICANT: Wagner, Fred W.
APPLICANT: Coolidge, Thomas R.
APPLICANT: Holmquist, Barton
TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
OPERATING SYSTEM: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5656456west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,166
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/091,751
FILING DATE:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 8648.35-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPR 3
Db 2 GPR 4

RESULT 42
US-08-457-166-11
; Sequence 11, Application US/08457166
; Patent No. 5656456
; GENERAL INFORMATION:
; APPLICANT: Stout, Jay
; APPLICANT: Wagner, Fred W.
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
; TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
; TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
; TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5656456west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/457,166
; FILING DATE: 13-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/091,751
; FILING DATE:
; APPLICATION NUMBER: US 07/912,798
; FILING DATE: 13-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 8648.35-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-457-166-11

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 2 GPR 4

RESULT 43
US-08-299-636-30
; Sequence 30, Application US/08299636
; Patent No. 5653041
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: KIRBY, Robert A.
; APPLICANT: DUNN-DUFAULT, Robert
; TITLE OF INVENTION: HYDRAZINO-TYPE RADIONUCLIDE CHELATORS
; TITLE OF INVENTION: HAVING AN N3S CONFIGURATION
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/299,636
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 534
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/092,911
; FILING DATE: 18-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/262/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-636-30

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 1 GPR 3

RESULT 44
US-08-279-155-30
; Sequence 30, Application US/08279155
; Patent No. 5662885
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: GOODBODY, Anne
; TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI, D. MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/08/279,155
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURRAY, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P8074-4005

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-279-155-30

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
DB 1 GPR 3

RESULT 45
US-08-464-456-28
Sequence 28, Application US/08464456
Patent No. 5681541
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
IMAGING
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,456
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5681541nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-456-28

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
DB 1 GPR 3

RESULT 46
US-08-470-220A-9

Sequence 9, Application US/08470220A
Patent No. 5707826
GENERAL INFORMATION:
APPLICANT: Wagner, Fred W.
APPLICANT: Stout, Jay
APPLICANT: Henriksen, Dennis
APPLICANT: Partridge, Bruce
APPLICANT: Manning, Shane
TITLE OF INVENTION: Enzymatic Method for Modification of
Recombinant Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 NO. 5707826west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,220A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/095,162
FILING DATE: 20-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,659
REFERENCE/DOCKET NUMBER: 8648.32-US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-220A-9

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
DB 2 GPR 4

RESULT 47
US-08-703-988A-30
Sequence 30, Application US/08703988A
Patent No. 5780005
GENERAL INFORMATION:
APPLICANT: POLIAK, Alfred
APPLICANT: GOODBODY, Anne
TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE
CHELATORS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY & ORAM
ADDRESSEE: LLP
STREET: 655 Fifteenth Street, N. W., Suite 330
STREET:
STREET: G Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA

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; ZIP: 20005-5701
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,988A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,155
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURRAY, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P8074-6011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-703-988A-30

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 48
US-08-463-052-28
; Sequence 28, Application US/08463052
; Patent No. 578960
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,052
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5788960nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1104-V
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 715 1000
; TELEFAX: 312 715 1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 28:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-463-052-28

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 49
US-08-480-551-28
; Sequence 28, Application US/08480551
; Patent No. 5811394
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,551
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/264,176
; FILING DATE:
; APPLICATION NUMBER: US 07/653,012
; FILING DATE: 08-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 90,1104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 715 1000
; TELEFAX: 312 715 1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-480-551-28

Query Match 72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 50
US-08-387-749-7

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; Sequence 7, Application US/08387749
; Patent No. 5814460
; GENERAL INFORMATION:
; APPLICANT: VENTON, DUANE L.
; APPLICANT: HOPFINGER, ANTON J.
; APPLICANT: LE BRETON, GUY
; TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
; TITLE OF INVENTION: USEFUL PEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,749
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08231
; FILING DATE: 09-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/932,200
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,315
; FILING DATE: 21-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00891
; FILING DATE: 14-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/480,865
; FILING DATE: 14-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: VENTON=1C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-387-749-7

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Query Match          72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Prad. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPR 3
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Db      1 GPR 3

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Search completed: September 7, 2004, 19:32:52
 Job time : 17 secs

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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:21:01 ; Search time 52 Seconds

(without alignments)
21.734 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPR 4

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 15518

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

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1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	25	100.0	4	2 AAR49796	Aar49796 Sequence
5	25	100.0	4	2 AAW09861	Aaw09861 Thrombin
6	25	100.0	4	2 AAW21198	Aaw21198 GPRP-pept
7	25	100.0	4	2 AAW34568	Aaw34568 Synthetic
8	25	100.0	4	2 AAW45491	Aaw45491 Targeting
9	25	100.0	4	2 AAW52073	Aaw52073 Sequence
10	25	100.0	4	2 AAY41677	Aay41677 Fibrin po
11	25	100.0	4	2 AAY31032	Aay31032 Non-cross
12	25	100.0	4	3 AAY32378	Aay32378 Cell diff
13	25	100.0	4	3 AAY54922	Aay54922 Fibrin po
14	25	100.0	4	3 AAB20589	Aab20589 Targeting
15	25	100.0	4	4 AAB98927	Aab98927 Acylated
16	25	100.0	4	5 ABG30381	Abg30381 Glycoprot
17	25	100.0	4	6 ABG74561	Abg74561 Oligopept
18	25	100.0	4	7 ABU63154	Abu63154 Targeting
19	25	100.0	4	7 ADD32227	Add32227 Fibrin po
20	22	88.0	4	2 AAR05861	Aar05861 Anti-coag
21	19	76.0	3	6 ABR55099	Abr55099 MMP subst
22	19	76.0	4	2 AAR05860	Aar05860 Anti-coag
23	19	76.0	4	2 AAR21664	Aar21664 Cyclic te
24	19	76.0	4	2 AAR80056	Aar80056 Peptidase
25	19	76.0	4	2 AAW51018	Aaw51018 Hirutinin

26	19	76.0	4	2 AAW94617	Aaw94617 Src homol
27	19	76.0	4	7 AAO29624	Aao29624 Anti-angi
28	19	76.0	4	7 ADC22266	Adc22266 Protein b
29	19	76.0	4	7 ADC15592	Adc15592 Rho 110 1
30	19	76.0	4	7 ADCL1585	Adcl1585 Rho 110 1
31	19	76.0	4	7 ADC15559	Adc15559 Rho 110 1
32	19	76.0	4	7 ADD52662	Add52662 Angiogen
33	18	72.0	3	3 AAY80482	Aay80482 Cell adhe
34	18	72.0	3	4 AAB91977	Aab91977 Fibrinect
35	18	72.0	3	6 ABU60858	Abu60858 Peptide p
36	18	72.0	4	2 AAR26394	Aar26394 Sequence
37	18	72.0	4	2 AAR32383	Aar32383 Fibrinoge
38	18	72.0	4	2 AAR32384	Aar32384 Fibrinoge
39	18	72.0	4	2 AAR32385	Aar32385 Fibrinoge
40	18	72.0	4	2 AAR48072	Aar48072 Biologica
41	18	72.0	4	2 AAR48079	Aar48079 Intra/Int
42	18	72.0	4	2 AAR49797	Aar49797 Sequence
43	18	72.0	4	2 AAR49798	Aar49798 Sequence
44	18	72.0	4	2 AAR49799	Aar49799 Sequence
45	18	72.0	4	2 AAR60327	Aar60327 Blood coa
46	18	72.0	4	2 AAW09862	Aaw09862 Thrombin
47	18	72.0	4	2 AAR80052	Aar80052 Peptidase
48	18	72.0	4	2 AAR80053	Aar80053 Peptidase
49	18	72.0	4	2 AAR69071	Aar69071 Interconn
50	18	72.0	4	2 AAW11088	Aaw11088 Thrombus-
51	18	72.0	4	2 AAW32859	Aaw32859 Thrombus-
52	18	72.0	4	2 AAW32851	Aaw32851 Thrombus-
53	18	72.0	4	2 AAW31139	Aaw31139 Thrombus-
54	18	72.0	4	2 AAW52391	Aaw52391 Beta-turn
55	18	72.0	4	2 AAW52392	Aaw52392 Beta-turn
56	18	72.0	4	2 AAW75467	Aaw75467 Mammalian
57	18	72.0	4	2 AAY09588	Aay09588 Antimicro
58	18	72.0	4	2 AAY09589	Aay09589 Antimicro
59	18	72.0	4	2 AAW92901	Aaw92901 Fibrinoge
60	18	72.0	4	2 AAW92899	Aaw92899 Fibrinoge
61	18	72.0	4	2 AAW92900	Aaw92900 Fibrinoge
62	18	72.0	4	2 AAY33405	Aay33405 Thrombin
63	18	72.0	4	3 AAB10630	Aab10630 Oligopept
64	18	72.0	4	4 AAB74836	Aab74836 Human min
65	18	72.0	4	4 AAW09059	Aaw09059 Human thr

ALIGNMENTS

RESULT 1				
AAP61324				
ID	AAP61324 standard; peptide; 4 AA.			
XX	AAP61324;			
AC				
XX				
DT	24-OCT-2003 (revised)			
DT	27-AUG-2003 (revised)			
DT	03-OCT-2002 (revised)			
DT	22-JUL-1991 (first entry)			
XX	Sequence of tetrapeptide of desAA-fibrin.			
DE	Tissue plasminogen activator; fibrinolysis; assay; diagnosis.			
KW	Coelognathus radiatus.			
XX	Bothrops; genus".			
OS	MO8605814-A.			
PN	09-OCT-1986.			
XX				
PD	27-MAR-1986; 86WO-SE000144.			
XX				
PF	01-APR-1985; 85SE-00001614.			
XX				
PR	(BIOP-) BIOPOOL AB.			
XX	(RANE/) RANEY M G.			
PA				

XX Ranby M;
 XX WPI; 1986-278827/42.
 XX Fibrin solubilised with tetra:peptide - used in diagnostic procedures for
 XX determining fibrinolysis factors.
 XX Claim 2; Page 18; 22pp; English.
 XX The patentors claim a compsn. in which AAP61324 is pref. present at a
 CC conc. of equal to or more than, 0.4 (pref. 2) mg./ml. of the compsn. The
 CC compsn. can be used in diagnostic tests such as the determ. of the
 CC enzyme tissue plasminogen activator as a standard in the detection of
 CC trace ants. of fibrin in biological fluids. It may also be administered
 CC in vivo to measure the total fibrinolytic capacity of an organism.
 CC (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 27-AUG-2003
 CC to correct OS field.) (Updated on 24-OCT-2003 to standardise OS field)
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 25; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 2
 AAR05320
 ID AAR05320 standard; peptide; 4 AA.
 XX AAR05320;
 XX 25-MAR-2003 (revised)
 DT 08-OCT-1990 (first entry)
 DT Anti-coagulant peptide.
 DE Anti-coagulant; cerebral thrombosis; myocardial infarction.
 KW Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 3
 FT FT Misc-difference 4 /label= ornithine.
 FT FT Misc-difference 4 /label= proline or prolylproline.
 FT JF02115197-A.
 FN 27-APR-1990.
 PD 21-OCT-1988; 88JP-00265809.
 PF 21-OCT-1988; 88JP-00265809.
 PR (DAUC) DAIICHI SEIYAKU CO.
 XX WPI; 1990-175285/23.
 DR Peptide contg. proline - is used for cerebral thrombosis, myocardial
 XX PT infarction etc. due to anti-coagulation activity.
 XX Claim 1; Page 975; 10pp; Japanese.
 XX C-terminal is in amide form. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 3
 AAR32382
 ID AAR32382 standard; peptide; 4 AA.
 XX AAR32382;
 AC 25-MAR-2003 (revised)
 DT 01-JUL-1993 (first entry)
 DT Fibrinogen binding peptide #6.
 DE platelet aggregation; fibrinogen A-alpha chain; protein scrambling;
 KW GPR-like peptide.
 XX Synthetic.
 OS WO9304079-A1.
 FN 04-MAR-1993.
 PD 20-AUG-1992; 92WO-US006933.
 PF 21-AUG-1991; 91US-00813315.
 PR (RECE-) RECEPTOR LAB INC.
 XX Venton DL, Hopfinger AJ, Le Breton G;
 PI WPI; 1993-093932/11.
 DR Identifying peptide(s) which bond to predetermined targets - by random
 PT degradation and recombination of peptide(s) and isolating bound
 PT peptide(s).
 XX Example 5; Page 58; 89pp; English.
 PS Synthetic peptides beginning with the sequence Gly-Pro-Arg (e.g. GPRP)
 CC will bind to fibrinogen and prevent fibrin polymerisation. A scrambling
 CC reaction was used to determine whether unique GPR-like peptides could be
 CC created from a reaction seeded with GPR and if these new products could
 CC bind to fibrinogen. See e.g. AAR32379. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 4
 AAR49796
 ID AAR49796 standard; peptide; 4 AA.
 XX AAR49796;
 AC 25-MAR-2003 (revised)
 DT 23-AUG-1994 (first entry)
 DT Sequence of peptide which binds to human fibrinogen.
 XX

XX Random degradation; recombination; scrambling reaction.
 XX Synthetic.
 OS WO9404558-A1.
 PN 03-MAR-1994.
 PD 09-AUG-1993; 93WO-US008231.
 PF 21-AUG-1992; 92US-00932200.
 XX (RECE-) RECEPTOR LAB INC.
 XX Venton DL, Hopfinger AJ;
 PI WPI; 1994-083103/10.
 DR Identifying peptides which binds to a specific target - by contacting
 XX target with scrambled equilibrium mixt. of many peptide derived from
 XX protein by incubation with protease, for detecting potential therapeutic
 XX agents.
 XX Example; Page 54; 97pp; English.
 XX The inventors claim a method for inexpensively and rapidly producing a
 CC large and varied population of peptides and screening this varied
 CC population for the presence of peptides which bind to a target, for
 CC example, a macromolecule associated with a particular physiological
 CC function. The specific binding peptides are isolated and sequenced,
 CC synthesised on a large-scale, their biological activity is demonstrated,
 CC and then subjected to clinical testing. The random population of peptides
 CC is generated by employing a scrambling system which utilises one or more
 CC proteases, esp. pepsin, papain, bromelain, thermolysin, trypsin, pronase,
 CC chymotrypsin, subtilisin and dipeptidyl peptidase IV. A typical starting
 CC protein is casein. Targets are esp. receptors involved in physiological
 CC processes, partic. fibrinogen, sickle cell haemoglobin, collagenase IV;
 CC rennin; Gp. IIB Iiia or phospholipase A2. It has been demonstrated that
 CC synthetic peptides beginning with the sequence GPR will bind to
 CC fibrinogen. Such peptides include GPR, GPRP and GPRV. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 5
 AAW09861
 ID AAW09861 standard; peptide; 4 AA.
 XX
 AC AAW09861;
 XX
 DT 30-JUN-1997 (first entry)
 XX
 DE Thrombin inhibitor.
 XX
 KW thrombin; inhibitor; aggregation; platelet; determination; assay;
 KW qualitative; quantitative; fibrin.
 XX
 OS Synthetic.
 XX
 XX EP661383-A2.
 PN 05-JUL-1995.
 PD

PF 15-DEC-1994; 94EP-00119803.
 XX
 PR 30-DEC-1993; 93DE-04344919.
 XX
 PA (BEHW) BEHRINGWERKE AG.
 XX
 PI Reers M;
 XX
 XX WPI; 1995-233339/31.
 DR
 XX Determn. of thrombin-induced platelet aggregation in presence of fibrin -
 PT comprises use of fibrin aggregation inhibitor to suppress fibrin clot
 PT formation.
 XX
 XX Claim 4; Col 5; 5pp; German.
 PS
 XX In the qualitative or quantitative determ. of thrombin-induced platelet
 CC aggregation in the presence of fibrin, interference from fibrin clot
 CC formation is suppressed with a fibrin-aggregation inhibitor (e.g.
 CC AAW09861-63). The assay may be used to determine the platelet aggregation
 CC inhibitory activity of thrombin inhibitors. The peptides inhibit fibrin
 CC clot formation at high thrombin concns. without inhibiting platelet
 CC aggregation
 XX
 XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 6
 AAW25198
 ID AAW25198 standard; peptide; 4 AA.
 XX
 AC AAW25198;
 XX
 DT 05-JAN-1998 (first entry)
 XX
 DE GPRP-peptide capable of binding cell adhesion molecules.
 XX
 XX GPRP; glycine; proline; arginine; proline; bladder irrigation;
 KW cell adhesion molecule; binding; tumour removal; endoscopic operation;
 KW transurethral resection; cancer; neoplasia.
 XX
 OS Synthetic.
 XX
 PN DE19529909-A1.
 XX
 PD 20-FEB-1997.
 XX
 PF 15-AUG-1995; 95DE-01029909.
 XX
 PR 15-AUG-1995; 95DE-01029909.
 XX
 XX (FREP) FRESENIUS AG.
 PA
 XX Boehle A;
 PI
 XX WPI; 1997-133793/13.
 DR
 XX Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
 PT adhesion molecules.
 PT
 XX Claim 9; Page 8; 8pp; German.
 PS
 XX AAW25198 and AAW25199 are peptides containing a GPRP sequence. The
 CC peptides are capable of binding to cell adhesion molecules and are used
 CC in aqueous irrigation solutions for use during and after endoscopic

CC operations. Preferred irrigation solutions are electrolyte-free and
 CC contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing
 CC the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KOAGDV
 CC and/or REDV (given in one letter amino acid code). The solutions are
 CC especially used for irrigating the bladder during and after tumour
 CC removal by transurethral resection. The peptides protect against
 CC recurrence of tumours
 XX
 XX Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 GPRP 4
 Db 1 GPRP 4

RESULT 7
 AAW34568
 ID AAW34568 standard; peptide; 4 AA.

XX AC AAW34568;

XX DT 05-MAR-1998 (first entry)

XX DE Synthetic fibrinogen binding peptide 1.

XX KW Fibrinogen binding peptide; fibrinopeptide A; fibrinogen isolation.

XX OS Synthetic.

XX PN WO9726280-A1.

XX PD 24-JUL-1997.

XX PF 14-JAN-1997; 97WO-AUG000013.

XX PR 16-JAN-1996; 96AU-00007564.

XX PS (CSLC-) CSL LTD.

XX PI Kanellos J, Pham H, Oates A, Goss N;

XX DR WPI; 1997-385298/35.

XX Recovery of fibrinogen using polysaccharide solid support coupled to
 fibrinogen-binding peptide - requires only mild elution buffers.

XX Claim 5; Page 14; 24pp; English.

XX Peptides AAW34568-71 are synthetic fibrinogen binding peptides. A
 CC tripeptide, Gly-Pro-Arg is also claimed. This tripeptide sequence
 CC corresponds to the first 3 amino acids of the alpha-chain exposed by the
 CC thrombin catalysed release of the fibrinopeptide A in all vertebrate
 CC species. In the present peptide, the addition of a proline residue at
 CC position 4 increases the affinity of the peptide for fibrinogen almost
 CC tenfold. These synthetic fibrinogen binding peptides are immobilised on a
 CC novel polysaccharide support (e.g. Sephadex) to which they are coupled
 CC through a spacer or linker moiety. This linker moiety comprises a chain
 CC of greater than 7 atoms. The solid support is useful for the recovery and
 CC isolation of fibrinogen from material such as plasma, plasma fractions
 CC and fibrinogen-containing cell culture media arising from the production
 CC of fibrinogen by recombinant DNA techniques. The process is superior to
 CC other known affinity isolation procedures in that only mild elution
 CC buffers are required to recover the bound fibrinogen
 XX

XX Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 Db 1 GPRP 4

RESULT 8
 AAW45491
 ID AAW45491 standard; peptide; 4 AA.

XX AC AAW45491;

XX DT 20-MAY-1998 (first entry)

XX DE Targeting ligand directed to the glycoprotein GPIIb/IIIa receptor.
 XX KW Contrast agent; targeted composition; diagnosis; diseased tissue;
 XX KW Glycoprotein GPIIb/IIIa receptor.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9640285-A1.

XX PD 19-DEC-1996.

XX PF 06-JUN-1996; 96WO-US009938.

XX PR 07-JUN-1995; 95US-00497684.

XX PR 01-MAY-1996; 96US-00640464.

XX PA (IMAR-) IMARX PHARM CORP.

XX PI Unger EC, Shen D, Wu G;

XX DR WPI; 1997-077233/07.

XX Contrast agent or targeted compen. for imaging or treating diseased
 tissue - comprising lipid, protein or polymer, a gas, and a targeting
 ligand e.g. a protein, peptide, saccharide or steroid.

XX Disclosure; Page 55; 175pp; English.

XX This sequence represents a targeting ligand directed to the GPIIb/IIIa
 CC receptor. The invention relates to a contrast agent for diagnostic
 CC imaging or a target composition which comprises: (i) a lipid, protein or
 CC polymer and (ii) a gas, in combination with (iii) a targeting ligand
 CC (Ti). Ti targets cells or receptors selected from myocardial,
 CC endothelial, epithelial and tumour cells and the glycoprotein GPIIb/IIIa
 CC receptor. Also claimed are: a composition comprising vesicles containing
 CC (i) - (iii) and an aqueous carrier; a targeted vesicle composition
 CC comprising a fluorinated gas and a targeting ligand (Ti) which targets
 CC tissues or receptors; a formulation for therapeutic or diagnostic use
 CC comprising (i)-(iii) and a bioactive agent; and a method for providing an
 CC image of an internal region of a patient, or for diagnosing the presence
 CC of diseased tissue, comprising: (a) administration of a composition as
 CC above; and (b) scanning the patient using ultrasound to obtain a visible
 CC image of the region or diseased tissue. The methods and compounds are
 CC useful for imaging or diagnosing the presence of diseased tissue,
 CC especially myocardial, endothelial or epithelial tissue but also
 CC gastrointestinal and cardiovascular regions. In particular the ligand
 CC targets regions of arteriosclerosis. Stabilised vesicles are particularly
 CC useful for perfusion imaging. The vesicles may also be used to deliver
 CC active agents to an intended target such as tissue or a receptor, and
 CC ultrasound can then be used to promote rupture of the vesicles and
 CC release a bioactive or diagnostic agent
 XX

XX Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 9
 AAW52073
 ID AAW52073 standard; peptide; 4 AA.
 AC AAW52073;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-SEP-1998 (first entry)
 XX
 XX Sequence contained in fibrin-specific targeting compound.
 DE Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
 KW thrombus.
 KW
 XX Synthetic.
 OS
 XX WO9824917-A1.
 PN
 XX 11-JUN-1998.
 PD
 XX 02-DEC-1997; 97WO-US021918.
 PF
 XX 02-DEC-1996; 96US-00753781.
 PR
 XX (DIAT-) DIATIDE INC.
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 FA
 XX Markland FS, Bush LR, Swenson S, Flores Sanchez E;
 PI WPI; 1998-333336/29.
 XX
 DR New thrombolytic agents - comprise thrombolytic proteinase covalently
 PT linked to targeting compound for binding to component of thrombus.
 PT
 XX Claim 9; Page 63; 79pp; English.
 PS
 XX The invention relates to new thrombolytic agents which comprise a
 CC thrombolytic proteinase covalently linked to a targeting compound capable
 CC of specifically binding to a component of a thrombus. The thrombolytic
 CC agents can be used for eliminating thrombi in vivo in, e.g. myocardial
 CC infarction, cerebral ischaemia, deep vein thrombosis or pulmonary
 CC embolism. A labelled form of the thrombolytic agent can also be used to
 CC image thrombi for diagnostic purposes. The thrombolytic agents are
 CC specifically targeted to thrombus sites in vivo and have minimal
 CC haemorrhagic side effects and side effects related to non-specific
 CC proteolysis. Multiple copies of the present amino acid sequence (GPRP)
 CC may be used in a fibrin-specific targeting compound. (Updated on 25-MAR-
 CC 2003 to correct PI field.)
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 10
 AAY41677
 ID AAY41677 standard; peptide; 4 AA.
 AC AAY41677;
 XX
 DT 07-DEC-1999 (first entry)
 DT
 XX

Fibrin polymerisation inhibitor peptide.
 Fibrin polymerisation inhibitor; factor Xa; thrombin; factor VIII;
 factor IX; factor X; coagulation factor; blood; photometric;
 Protein C anticoagulant pathway; thromboembolic disease;
 deep venous thrombosis; pulmonary embolism.
 Synthetic.
 OS
 XX WO9947699-A1.
 PN
 XX 23-SEP-1999.
 PD
 XX 11-MAR-1999; 99WO-EP001599.
 PF
 XX 19-MAR-1998; 98EP-00105043.
 PR
 XX (CHRO-) CHROMOGENIX AB.
 PA
 XX Rosen BS, Hall CMY;
 PI WPI; 1999-571846/48.
 DR
 XX New assays for determination of activity of components in the Protein C
 PT anticoagulant pathway, used for the study of diseases such as deep venous
 PT thrombosis and pulmonary embolism.
 PT
 XX Claim 27; Page 50; 67pp; English.
 PS
 XX Assays have been developed for the determination of activity of
 CC components in the Protein C anticoagulant pathway using additional metal
 CC ions to improve the sensitivity of the assays. An in vitro photometric
 CC method for qualitative screening and quantitative determination of the
 CC functional activity of components of the Protein C anticoagulant pathway
 CC of blood coagulation, comprises measuring the conversion rate of an
 CC exogenous substrate by an enzyme. The activity of the enzyme is related
 CC to the Protein C anticoagulant activity, in a blood sample of a human
 CC comprising coagulation factors and the exogenous substrate after at least
 CC partial activation of coagulation through the intrinsic, extrinsic, or
 CC common pathway and triggering coagulation by: (1) adding calcium ions;
 CC and (2) comparing the conversion rate with the conversion rate of a
 CC normal human blood sample determined in the same way, characterized by
 CC adding further metal(s) ions selected from divalent metal ions and
 CC monovalent copper ions to the sample. The method can be used for the
 CC global screening for defects in the Protein C anticoagulant pathway of
 CC blood coagulation, for determination of free Protein S activity in a
 CC blood sample, for determination of Protein C activity in a blood sample,
 CC and for screening for Factor V mutations in a blood sample. It allows
 CC improved screening and diagnosing of defects in the Protein C
 CC anticoagulant pathway in investigation of patients with thromboembolic
 CC diseases such as deep venous thrombosis and/or pulmonary embolism. The
 CC present sequence represents a fibrin polymerisation inhibitor for use in
 CC a method described in the present invention
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 11
 AAY31032
 ID AAY31032 standard; peptide; 4 AA.
 XX
 AC AAY31032;
 XX
 DT 21-OCT-1999 (first entry)
 DT
 XX

DE Non-crosslinked protein particle peptide 81.
 XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KW albumin; haemoglobin; nanometer; micrometer; clearance.
 XX Synthetic.
 OS
 XX US5945033-A.
 PN
 XX 31-AUG-1999.
 PD
 XX 12-NOV-1996; 96US-00747137.
 PF
 XX 15-JAN-1991; 91US-00641720.
 PR
 XX 13-OCT-1992; 92US-00959560.
 PR
 XX 01-JUN-1993; 93US-00069831.
 PR
 XX 14-MAR-1994; 94US-00212546.
 PR
 XX (HEMO-) HEMOSPHERE INC.
 PA
 XX Yen RCK;
 PI
 XX WPI; 1999-508153/42.
 DR
 XX Non-crosslinked protein particles for therapeutic and diagnostic use.
 PT
 XX Example 22; Col 83-84; 65pp; English.
 PS
 XX This invention describes a novel aqueous suspension of monodisperse
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
 CC stable against dissolving upon dilution with an alcohol-free aqueous
 CC medium. The method involves (a) forming an aqueous solution containing
 CC albumin and hemoglobin and (b) treating the aqueous solution with an
 CC alcohol to cause the solution to become turbid. The particles are useful
 CC as agents for in vivo administration, either of their own administration
 CC or as a vehicle for other therapeutic or diagnostic agents. The method
 CC permits the formation of albumin and hemoglobin particles in the
 CC nanometer and micrometer size range, in a form closer to their natural
 CC form than the forms of the prior art. The particles therefore constitute
 CC a more closely controlled agent for in vivo administration, with greater
 CC ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GPRP 4
 Db 1 GPRP 4
 RESULT 12
 AAY32378
 ID AAY32378 standard; peptide; 4 AA.
 AC
 XX AAY32378;
 XX
 XX 28-FEB-2000 (first entry)
 DT
 XX Cell differentiation, proliferation and maintenance factor peptide.
 DE
 XX Cell differentiation; cell proliferation; cell maintenance;
 KW ectoderm-like cell; embryonic stem cell; pluripotent cell; gene therapy;
 KW cell therapy; tissue transplant; organ transplant; xeroderma; xeroderma;
 KW allotransplant; concomitant transplantation; transgenic animal.
 XX
 OS Synthetic.
 XX WO9953021-A1.
 PN
 XX

PD 21-OCT-1999.
 XX 09-APR-1999; 99WO-AU000265.
 PF
 XX 09-APR-1998; 98AU-00002912.
 PR
 XX 23-SEP-1998; 98AU-00006097.
 PR
 XX (BRES-) BRESAGEN LTD.
 PA
 XX Bettess MD, Rathjen PD, Rathjen J;
 PI
 XX WPI; 2000-061970/05.
 DR
 XX New isolated biologically active factor capable of influencing
 PT differentiation, proliferation or maintenance of pluripotent cells.
 PT
 XX Claim 3; Page 122; 189pp; English.
 PS
 XX This sequence represents a peptide that can form the low mol.wt.
 CC component of a novel biologically active factor that is capable of
 CC influencing the differentiation, proliferation and/or maintenance of
 CC pluripotent cells. The factor consists of a low mol.wt. component
 CC selected from Pro, Pro-Ala, Ala-Pro-Gly, Pro-OH-Pro, Gly-Pro-
 CC Ala, Gly-Pro-OH-Pro, a peptide given in AAY32378-82, or a protease
 CC digested (including collagenase digested) collagen fragment, and a high
 CC mol.wt. component such as fibronectin. The biologically active factor is
 CC obtained from conditioned media of hepatic or hepatoma cells or cell
 CC lines or extraembryonic endodermal cells or cell lines. The factor is
 CC capable of causing the transition of pluripotent cells (e.g. embryonic
 CC stem cells in adherent culture and in suspension culture) to pluripotent
 CC cells having different properties, more specifically primitive ectoderm-
 CC like (EPL) cells. The factor is also capable of maintaining and
 CC supporting proliferation of these cells in vitro. It also allows the
 CC isolation and maintenance of EPL cells derived from in vitro and in vivo
 CC primitive ectoderm. These cells can be used in allo-, concomitant- or
 CC xeno-transplantation, cell therapy, tissue and organ augmentation or
 CC replacement, and gene therapy. They can also be used for producing
 CC chimeric or transgenic animals
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 25; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GPRP 4
 Db 1 GPRP 4
 RESULT 13
 AAY54922
 ID AAY54922 standard; peptide; 4 AA.
 AC
 XX AAY54922;
 XX
 XX 15-FEB-2000 (first entry)
 DT
 XX Fibrin polymerisation site.
 DE
 XX Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m;
 KW GPIIb/IIIa receptor; cyclic peptide ligand.
 KW
 XX Synthetic.
 OS
 XX US5968476-A.
 PN
 XX 19-OCT-1999.
 PD
 XX 07-JUN-1995; 95US-00484773.
 PF
 XX 21-MAY-1992; 92US-00886052.
 PR
 XX 11-JUL-1994; 94US-00273274.
 PR

XX PA (DIAT-) DIATIDE INC.
XX FI Dean RT, Lister-James J;
XX DR WPI; 2000-021733/02.
XX PT A complex used for thrombus imaging comprises technetium-99m complexed
XX with a peptide ligand for GPIIb/IIIa receptor.
XX FS Claim 7; Col 31-32; 18pp; English.
XX CC This sequence represents the fibrin polymerisation site. The invention
XX relates to a complex (A) for thrombus imaging comprises technetium-99m
XX (Tc-99m) complexed with a reagent comprising a peptide (P) with 4 to 100
XX amino acids sequence and a Tc-99m binding moiety covalently bound to (P).
XX (P) is selected from a linear peptide ligand for a GPIIb/IIIa receptor
XX not comprising the amino acid sequence (arginine-glycine-aspartate), a
XX peptide ligand for a polymerisation site of fibrin, and a cyclic peptide
XX ligand for the GPIIb/IIIa receptor. The thrombus imaging reagents
XX provided by the present invention can be used for visualising thrombi in
XX a mammalian body when Tc-99m is labelled
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
RESULT 14
AAB20589
ID AAB20589 standard; peptide; 4 AA.
XX AC AAB20589;
XX DT 12-DEC-2000 (first entry)
XX DE Targeting ligand peptide #5.
XX KW Targeting ligand peptide; imaging; ultrasound; vesicle; tumour;
XX myocardial; endothelial; epithelial; glycoprotein GPIIb/IIIa receptor;
XX detection; thrombus; integrin; malignancy; inflammation; lesion;
XX atherosclerotic plaque; carcinoma.
XX OS Synthetic.
XX PN WO200045856-A2.
XX FD 10-AUG-2000.
XX PF 02-FEB-2000; 2000WO-US002620.
XX PR 03-FEB-1999; 99US-00243640.
XX PA (IMAR-) IMARX PHARM CORP.
XX PI Ungr EC, Wu Y;
XX DR WPI; 2000-532867/48.
XX PT Ultrasound method, useful for diagnosis of e.g. thrombi or carcinomas,
XX PT uses different types of energy for priming and interrogating the subject.
XX PS Disclosure; Page 68; 211pp; English.
XX CC The present invention describes an ultrasound method comprising: (i)
XX administering a targeted vesicle composition (A); and (ii) scanning the
XX subject by exposure to a first type of ultrasound energy and then

CC interrogating with a second type of ultrasound energy. (A) consists of a
CC vesicle comprising a lipid, protein or polymer, encapsulating a gas, in
CC combination with a targeting ligand. The method is used to detect: (i) a
CC thrombus (particularly old or echogenic); (ii) a low concentration of
CC vesicles; or (iii) vesicles targeted to endothelial tissue, particularly
CC those containing integrins associated with malignancy or inflammation in
CC early or small lesions, e.g. atherosclerotic plaque or ovarian,
CC endometrial or other carcinomas. The method increases the signal from
CC microbubbles and reduces background noise. The present sequence
CC represents a targeting ligand peptide which is used in the method of the
XX present invention
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
RESULT 15
AAB98927
ID AAB98927 standard; peptide; 4 AA.
XX AC AAB98927;
XX DT 14-AUG-2001 (first entry)
XX DE Acylated amino protecting method fibrinogen peptide.
XX KW Acylated amino protection; chemical synthesis; drug delivery;
XX bioavailability; biostability.
XX OS Synthetic.
XX PN WO200125170-A1.
XX PD 12-APR-2001.
XX PF 16-AUG-2000; 2000WO-US040671.
XX PR 04-OCT-1999; 99US-0157435P.
XX PR 30-JUN-2000; 2000US-00609565.
XX PA (UYCA-) UNIV CALIFORNIA SAN DIEGO.
XX PI Goodman M, Creighton CJ;
XX DR WPI; 2001-389649/41.
XX PT New protected amino-substituted compounds bearing acylated N-methyl-alpha
XX -aminoisobutyryl moiety as amino protecting group, useful e.g. in organic
XX synthesis and in the formulation/delivery of prodrugs with improved
XX bioavailability.
XX PS Disclosure; Page 12; 39pp; English.
XX CC The present invention describes protected amino-substituted compounds
XX with an acylated N-methyl-alpha-aminoisobutyryl (NMeAib) moiety as the
XX amino protecting group. These can be used in chemical synthesis and in
XX drug delivery. They can be used as prodrugs which have improved
XX bioavailability or bioavailability. The present sequence is a peptide
XX described in the exemplification of the invention
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
Db 1 GPRP 4

RESULT 16
ABG30381
ID AEG30381 standard; peptide; 4 AA.
XX AC ABG30381;
XX AC ABG30381;
DT 07-OCT-2002 (first entry)
XX
XX Glycoprotein GPIIb/IIIa receptor targeting ligand #3.
DE Target vesicle; diagnostic imaging; thrombus; cancer; arteriosclerosis;
KW atherosclerotic plaque; infarcted myocardium;
KW glycoprotein GPIIb/IIIa receptor.
XX Synthetic.
OS
XX WO200236161-A2.
XX
XX 10-MAY-2002.
XX
XX 17-OCT-2001; 2001WO-US032308.
XX
XX 30-OCT-2000; 2000US-00699679.
XX
XX (IMAR-) IMARX THERAPEUTICS INC.
XX
XX Unger EC, Matsunaga TO, Schumann PA;
PI
XX WPI; 2002-489986/52.
XX
XX New targeted compound useful in target vesicle composition for imaging a
PT thrombus in a region of a patient has a combination of hydrophobic
PT compound, hydrophilic polymer and targeting ligand.
XX
XX Disclosure; Page 65; 206pp; English.
XX
XX This invention relates to a novel targeted compound having a combination
CC of hydrophobic compound, hydrophilic polymer and targeting ligand. The
CC invention also comprises a target vesicle composition comprising lipid,
CC protein or polymer gas filled vesicles in an aqueous carrier, a method
CC for imaging a thrombus in a region of a patient involving administering
CC to the patient a target vesicle composition and scanning the region
CC (preferably cardiac region) with diagnostic imaging (preferably
CC diagnostic ultrasound) and a method for lysing a thrombus in a blood
CC vessel. The invention also comprises a method for providing an image of
CC an internal region of a patient which can be used to obtain a visible
CC image of a region (preferably arteriosclerosis, atherosclerotic plaque,
CC infarcted myocardium or a cancer cell) and a method for diagnosing the
CC presence of disease tissue in a patient involving administering a target
CC vesicle composition and scanning the patient using ultrasound to obtain a
CC visible image of the region. The methods of the invention may be used for
CC imaging a thrombus in a region of a patient, lysing a thrombus in a blood
CC vessel, diagnosing the presence of diseased tissue in a patient and for
CC the therapeutic delivery in vivo of a bioactive agent. The compounds of
CC the invention are easily synthesised and have diagnostic efficacy, prior
CC enhanced biocompatibility and/or improved targeting efficacy over prior
CC art methods. The present sequence represents a targeting ligand to the
XX glycoprotein GPIIb/IIIa receptor used in the method of the invention
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 GPRP 4
|||||
Db 1 GPRP 4

RESULT 17
ABG74561
ID ABG74561 standard; peptide; 4 AA.
XX
XX AC ABG74561;
XX AC ABG74561;
DT 24-APR-2003 (first entry)
XX
XX Oligopeptide fragment #2.
DE
XX Cytostatic; antibacterial; tumour cell adhesion inhibitor; vaccine;
KW bladder carcinoma; transurethral resection; antimicrobial;
KW human medicine; veterinary medicine.
XX Unidentified.
XX DE10123348-A1.
XX
XX 21-NOV-2002.
XX
XX 14-MAY-2001; 2001DE-01023348.
XX
XX 14-MAY-2001; 2001DE-01023348.
XX
XX (PREP) PRESENTIUS KABI DEUT GMBH.
XX
XX Dormann D, Eichner W, Sommermeyer K, Volker L;
PI
XX WPI; 2003-168758/17.
XX
XX New DNA construct encoding polypeptide that includes cleavage sites,
PT useful for preparation of pharmaceutical peptides or their mixtures.
XX
XX Disclosure; Page 3; 12pp; German.
XX
XX This invention describes a novel DNA construct encoding a polypeptide
CC comprising several oligopeptide units and including recognition sites for
CC peptide cleavages. The products of the invention have cytostatic and
CC antibacterial activity, inhibit tumour cell adhesion and can be used to
CC prepare vaccines. The constructs are used for recombinant production of
CC peptides or their mixtures for use as pharmaceuticals, e.g. a mixture of
CC peptides used, in a rinse solution, to reduce the high rate of relapse in
CC superficial bladder carcinoma after transurethral resection or as
CC antimicrobial peptides for control of antibiotic-resistant bacteria in
CC human or veterinary medicine. The constructs allow the possible
CC production of peptides, or specific mixtures of them, at high
CC concentration and reduced cost. This sequence represents an oligopeptide
CC described in the disclosure of the invention
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 25; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 GPRP 4
|||||
Db 1 GPRP 4

RESULT 18
ABU63154
ID ABU63154 standard; peptide; 4 AA.
XX
XX AC ABU63154;
XX
XX DT 17-SEP-2003 (first entry)
XX
XX Targeting ligand #4 used in novel diagnostic ultrasound method.
XX
XX Ultrasound method; targeted vesicle composition; targeting ligand;


```

XX FH Key Location/Qualifiers
XX FT Misc-difference 3 /label= ornithine.
XX FT Misc-difference 4 /label= proline or prolylproline.
XX PN JP02115197-A.
XX PD 27-APR-1990.
XX PF 21-OCT-1988; 88JP-00265809.
XX PR 21-OCT-1988; 88JP-00265809.
XX PA (DAUC ) DAIICHI SEIYAKU CO.
XX DR WPI; 1990-175285/23.
XX
XX Peptide contg. proline - is used for cerebral thrombosis, myocardial
XX infarction etc. due to anti-coagulation activity.
XX PS Claim 1; Page 975; 10pp; Japanese.
XX CC C-terminal is in amide form. (Updated on 25-MAR-2003 to correct PA
XX field.)
XX SQ Sequence 4 AA;

Query Match 88.0%; Score 22; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB ||:|
1 GPRP 4

RESULT 21
ABR55099
ID ABR55099 standard; peptide; 3 AA.
XX AC ABR55099;
XX DT 02-JUL-2003 (first entry)
XX DE MMP substrate cleavage related peptide SEQ ID NO:101.
XX KW Matrix metalloproteinase; MMP-2; MMP-9; MT1-MMP; substrate; cytostatic;
XX peptidomimetic; antiinflammatory; neuroprotective; gene therapy;
XX tumour angiogenesis; inflammatory disease; neurodegenerative disease.
XX OS Synthetic.
XX PN WO2003025125-A2.
XX PD 27-MAR-2003.
XX PF 13-SEP-2002; 2002WO-US029060.
XX PR 14-SEP-2001; 2001US-00953592.
XX PA (BURN-) BURNHAM INST.
XX PI Smith JW, Chen EI, Kridel SJ;
XX WPI; 2003-354595/33.
XX
XX New isolated matrix metalloproteinase-2 (MMP-2), MMP-9, MT1-MMP selective
XX substrate polypeptide, useful for diagnosing and treating tumor
XX angiogenesis, inflammatory or neurodegenerative diseases.
XX PS Disclosure; Page 68; 146pp; English.

XX The present invention describes an isolated matrix metalloproteinase-2
XX (MMP-2), MMP-9 or MT1-MMP selective substrate polypeptide (I), or its
XX functional peptidomimetic. Also described is a method for preferentially
XX directing a moiety to a site of MMP-2, MMP-9 or MT1-MMP activity by
XX administering (i) to the subject. (i) have cytostatic, antiinflammatory
XX and neuroprotective activities, and can be used in gene therapy. The
XX polypeptides and methods from the present invention can be used for
XX diagnosing and treating tumour angiogenesis, inflammatory or
XX neurodegenerative diseases. ABR54999 to ABR55122 and ACC49718 to ACC49722
XX represent sequences used in the exemplification of the present invention
XX SQ Sequence 3 AA;

Query Match 76.0%; Score 19; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
DB |||
1 PRP 3

RESULT 22
AAR05860
ID AAR05860 standard; protein; 4 AA.
XX AC AAR05860;
XX DT 25-MAR-2003 (revised)
XX DT 08-OCT-1990 (first entry)
XX DE Anti-coagulant peptide.
XX KW Anti-coagulant; cerebral thrombosis; myocardial infarction.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 3 /label= ornithine.
XX FT Misc-difference 4 /label= proline or prolylproline.
XX PN JP02115197-A.
XX PD 27-APR-1990.
XX PF 21-OCT-1988; 88JP-00265809.
XX PR 21-OCT-1988; 88JP-00265809.
XX PA (DAUC ) DAIICHI SEIYAKU CO.
XX DR WPI; 1990-175285/23.
XX
XX Peptide contg. proline - is used for cerebral thrombosis, myocardial
XX infarction etc. due to anti-coagulation activity.
XX PS Claim 1; Page 975; 10pp; Japanese.
XX CC C-terminal is in amide form. (Updated on 25-MAR-2003 to correct PA
XX field.)
XX SQ Sequence 4 AA;

Query Match 76.0%; Score 19; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
DB |||
2 PRP 4

```

RESULT 23
AAR21664
ID AAR21664 standard; peptide; 4 AA.

XX AC AAR21664;
XX DT 17-JUN-1992 (first entry)
XX DE Cyclic tetrapeptide for tumour treatment (1).
XX KW Infection; virus; bacteria; fungi; autoimmune disease; cyclic.
XX OS Synthetic.
XX PN JP04021698-A.
XX PD 24-JAN-1992.
XX PF 11-MAY-1990; 90JP-00122290.
XX PR 11-MAY-1990; 90JP-00122290.
XX PA (BANY) BANYU PHARM CO LTD.
XX DR WPI; 1992-076791/10.
XX PT New cyclic tetra-peptide(s) useful for treatment of tumours, etc. -
XX FT prep'd. by cyclisation reaction with condensing agent e.g.
XX PS di:cyclo:hexyl:carbodiimide in presence of base.
XX SQ Claim 2; Page 1; 12pp; Japanese.

CC The peptide is useful for treatment of tumours, infections caused by
CC virus, bacteria or fungi, or autoimmune disease. It can be administered
CC orally or parenterally at daily dose of 1-500 mg. (p.o.) for adults. The
CC cyclisation is effected with a condensing agent in a solvent opt. in the
CC presence of a base at -50 degrees C to 50 degrees C for 30 minutes to 2
CC days
XX SQ Sequence 4 AA;
Query Match 76.0%; Score 19; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRP 4
DB 1 PRP 3

RESULT 24
AAR80056
ID AAR80056 standard; peptide; 4 AA.
XX AC AAR80056;
XX DT 25-APR-1996 (first entry)
XX DE Peptidase substrate #10.
XX KW Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
XX KW cerebral function.
XX OS Synthetic.
XX PN JP07227281-A.
XX PD 29-AUG-1995.
XX PF 15-FEB-1994; 94JP-00042027.
XX

XX PR 15-FEB-1994; 94JP-00042027.
XX (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
XX (NIHA-) NIPPON HAM KK.
XX WPI; 1995-331519/43.
XX 140 kDa peptidase hydrolyses proline rich proteins - useful for
XX prevention and treatment of diseases related to proline rich proteins and
XX studies of cerebral functions.
XX Example 4; Page 6; 7pp; Japanese.
XX The sequences represented by AAR80046 and AAR80048-R80059 are substrates
XX for the novel peptidase of the invention. The peptidase hydrolyses P-P-P-
XX P, P-P-P, and P-P and recognises the proline at the second residue from
XX the N-terminal of a peptide to release the N-terminal amino acid. The
XX enzyme's activity is stimulated with MnCl2 and inhibited with o-
XX phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
XX hydrolysis of proline containing physiologically active peptides,
XX oligoproline and proline rich proteins in the living body, particularly
XX in the brain of mammals. The peptidase is useful for the prevention and
XX treatment of proline rich protein related diseases and study of cerebral
XX functions
XX SQ Sequence 4 AA;
Query Match 76.0%; Score 19; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRP 4
DB 1 PRP 3

RESULT 25
AAW51018
ID AAW51018 standard; peptide; 4 AA.
XX AC AAW51018;
XX DT 04-AUG-1998 (first entry)
XX DE Hirutinin-2, a thrombin catalytic site inhibitor.
XX KW Thrombin inhibitor; catalytic site; fibrinogen gamma chain; gamma' chain;
XX KW thrombin exocite; hirutinin-2.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Modified-site 1 /note= "D-form residue, N-terminal acetyl"
XX FT WO9812318-A1.
XX PN 26-MAR-1998.
XX PD 13-JUN-1997; 97WO-US010429.
XX PF 17-SEP-1996; 96US-00713885.
XX PR (WISC) WISCONSIN ALUMNI RES FOUND.
XX PA Mosesson MW, Meh DA;
XX PI WPI; 1998-217260/19.
XX DR Thrombin inhibitor useful for inhibition of thrombin-mediated functions -
XX comprises a means for inactivating or sequestering thrombin and portion
XX of fibrinogen chain that binds at the anion-binding exosite of thrombin.
XX

PS Disclosure; Page 7; 37pp; English.

XX The invention relates to a new thrombin inhibitor which comprises: (a) a
CC means for inactivating or sequestering thrombin, and (b) a portion of the
CC fibrinogen gamma' chain that binds at the anion-binding exosite of
CC thrombin. Also claimed is a recombinant genetic construct comprising
CC nucleic acid sequences encoding the inhibitor above. The inhibitor
CC comprises three segments, the first binds to the catalytic site of
CC thrombin, the second connects the first and third segments, and the third
CC comprises a portion of the fibrinogen gamma' chain that binds to the
CC thrombin exosite. The third segment is preferably amino acids 414-427 of
CC the native human fibrinogen gamma' sequence. The inhibitor is useful for
CC the inhibition of thrombin-mediated functions in a patient or in
CC extracorporeal blood. The present sequence represents a thrombin
CC catalytic site inhibitor, hirutinin-2
XX

SQ Sequence 4 AA;

Query Match 76.0%; Score 19; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
Db 2 PRP 4

RESULT 26
AAW94617
ID AAW94617 standard; peptide; 4 AA.

AC AAW94617;

DT 29-APR-1999 (first entry)

DE Src homology 3 domain peptide mimetic tetrapeptide #1.

XX Src homology 3 domain; SH3 domain; peptidomimetic; mimetic; modulator;
KW beta-turn template; spiro[pyrrolidine-2':3'-piperidin-2-ones];
KW fused ring analogue; signal transduction protein interaction;
KW inhibit cell growth; infection; cancer.

XX Synthetic.

XX Key Location/Qualifiers
FH Modified-site 1 /note= "acetylated"

FT WO9854208-A1.

PD 03-DEC-1998.

XX 28-MAY-1998; 98WO-US010861.

PF 28-MAY-1997; 97US-00864241.

PR 18-MAY-1998; 98US-0085889P.

XX (CADU-) CADUS PHARM CORP.
XX Castelhano AL, Witter DJ;

DR WPI; 1999-080804/07.

XX spiro[pyrrolidine-2':3'-piperidin-2-ones] and their fused ring analogues -
FT used, e.g. to modulate signal transduction protein interactions, inhibit
PT cell growth and for use in treating infections and cancer.

XX Claim 3; Page 62; 73pp; English.

XX The present invention describes spiro[pyrrolidine-2':3'-piperidin-2-ones],
CC their fused ring analogues, and salts of both, all as individual
CC compounds or their libraries. They are peptidomimetics, and interact with
CC protein Src homology 3 (SH3) domains, involved in protein-protein

CC interactions in signal transduction. They cause disruption of the pathway
CC ; in particular, they inhibit the protein tyrosine kinase system involved
CC in cell growth regulation. The cells may be microbial, e.g. pathogenic
CC bacterial or fungal cells responsible for infections, or of transformed
CC cells, e.g. responsible for neoplastic conditions. Specific examples of
CC Src proteins with SH3 domains are those known by the abbreviations p85,
CC Fyn, Lyn, Hck, Syk, Grb2, Gap, STAT, p47-phox, p67-phox, and Prk. The
CC present sequence represents a tetrapeptide used in a spiro[pyrrolidine-
XX 2':3'-piperidin-2-ones] of the present invention

SQ Sequence 4 AA;

Query Match 76.0%; Score 19; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
Db 1 PRP 3

RESULT 27

AAO29624

ID AAO29624 standard; peptide; 4 AA.

XX AAO29624;

DT 27-AUG-2003 (first entry)

DE Anti-angiogenic peptide #11.

XX Anti-angiogenic; angiogenesis; cancer; autoimmune disease;
KW rheumatoid arthritis; immune arthritis; degenerative arthritis;
KW ocular disease; diabetic retinopathy; skin disease; psoriasis;
KW blood vessel disease; haemangioma; Crohn's disease; atherosclerosis;
KW keloid; ulcer; tumour; birth control agent.

XX Synthetic.

XX Key Location/Qualifiers

FH Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 4 /note= "C-terminal ethyl amide"

FT WO2003037912-A2.

XX 08-MAY-2003.

XX 30-OCT-2002; 2002WO-US034829.

XX 31-OCT-2001; 2001US-00999828.

XX (ABBO) ABBOTT LAB.

XX Haviv F, Bradley MF;

XX WPI; 2003-493204/46.

XX New compounds with anti-angiogenic activity, useful for inhibiting
PT angiogenesis, treating conditions that arise from, or are exacerbated by,
PT angiogenesis, e.g. cancer or autoimmune diseases, or preventing
PT metastases from tumors.

XX Claim 9; Page 31; 41pp; English.

XX The invention relates to peptides with anti-angiogenic activity. The
CC peptides of the invention are useful for inhibiting angiogenesis, for
CC treating conditions that arise from, or are exacerbated by, angiogenesis
CC such as cancer, autoimmune diseases (e.g. rheumatoid, immune and
CC degenerative arthritis), ocular diseases (e.g. diabetic retinopathy), skin
CC diseases (e.g. psoriasis), blood vessel diseases (e.g. haemangiomas),
CC Crohn's disease, atherosclerosis, keloids, or ulcers, or for preventing

CC metastases from the tumours. The peptides are also useful as birth
CC control agents, by inhibiting ovulation and establishment of placenta, or
CC for reducing bleeding. The present sequence is an example of peptide of
CC the invention
XX
SQ Sequence 4 AA;
Query Match 76.0%; Score 19; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRP 4
Db 2 PRP 4
|||
|||
RESULT 28
ADC22266
ID ADC22266 standard; peptide; 4 AA.
XX
AC ADC22266;
XX
DT 18-DEC-2003 (first entry)
XX
DE Protein binding domain amino acid sequence SEQ ID NO:115.
XX
KW recombinant fusion protein; fusion protein; binding; detection;
KW localisation domain; binding domain;
KW subcellular compartment localisation.
XX
OS Homo sapiens.
XX
PN WO2003012068-A2.
XX
PD 13-FEB-2003.
XX
PF 01-AUG-2002; 2002WO-US024572.
XX
PP 01-AUG-2001; 2001US-0309395P.
XX
PR 13-DEC-2001; 2001US-0341589P.
XX
PA (CELL-) CELLOMICS INC.
XX
PI Bright G, Premkumar DR, Chen Y;
XX
DR WPI; 2003-248174/24.
XX
DR N-PSDB; ADC22267.
XX
PT New recombinant fusion protein comprising detection and first
PT localization domains and a binding domain for the molecule of interest,
PT useful for detecting binding of a molecule of interest.
XX
PS Claim 8; SEQ ID NO 115; 101pp; English.
XX
CC The present invention describes a recombinant fusion protein (I) for
CC detecting binding of a molecule of interest. (I) comprises: (a) a
CC detection domain; (b) a first localisation domain; and (c) a binding
CC domain for the molecule of interest. The detection domain, the first
CC localisation domain and the binding domain for the molecule of interest
CC constituting the recombinant fusion protein for detecting binding of a
CC molecule of interest are operably linked. The binding domain for the
CC molecule of interest is separated from the first localisation domain by 0
CC 20 amino acid residues. The first localisation domain and the binding
CC domain for the molecule of interest both do not occur in a single non-
CC recombinant protein with the same spacing as in the recombinant fusion
CC protein for detecting binding of a molecule of interest. Also described:
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
CC (2) a recombinant expression vector comprising the nucleic acid control;
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
CC genetically engineered host cell transfected with the recombinant
CC expression vector; (4) a kit for detecting binding of the molecule of
CC interest; and (5) a method for identifying compounds that alter the
CC binding of the molecule of interest. The recombinant fusion protein is

CC useful for detecting binding of a molecule of interest. The recombinant
CC fusion protein eliminates the need to construct two or more chimeric
CC proteins and enables the monitoring of biochemical events in live, intact
CC or fixed cells. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 4 AA;
Query Match 76.0%; Score 19; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRP 4
Db 2 PRP 4
|||
|||
RESULT 29
ADC15592
ID ADC15592 standard; peptide; 4 AA.
XX
AC ADC15592;
XX
DT 18-DEC-2003 (first entry)
XX
DE Rho 110 labelled leaving group peptide #48.
XX
KW Assay; binding; target; analyte; enzyme activity.
XX
OS Synthetic.
XX
PN WO2003067212-A2.
XX
PD 14-AUG-2003.
XX
PF 21-JAN-2003; 2003WO-US001497.
XX
PP 08-FEB-2002; 2002US-00071395.
XX
PA (BECI) BECKMAN COULTER INC.
XX
PI Bell ML;
XX
DR WPI; 2003-689583/65.
XX
PT Assaying target analytes in a sample comprises determining the extent of
PT binding between the target analyte and the solid support-bound ligand of
PT the analyte useful for conducting multiplexed assays of multiple
PT analytes.
XX
PS Disclosure; Page 33; 48pp; English.
XX
CC The invention relates to a method for assaying target analyte(s). The
CC steric interference is provided by a solid support (s1). The method
CC involves assaying target analyte(s) (A) in a sample comprises providing
CC (A) and binding ligand (1) of (A) bound to a solid support, where the
CC support is porous, the ligand is bound within the pores of the support
CC ability, and the pores sterically interfere with the ability of the
CC binding ligand to bind to (A) that does not hinder the binding of all
CC other target analyte(s) to all other binding ligand(s). The method is
CC efficiently capable of simultaneously assaying multiple different
CC analytes and permits each target analyte to be assayed within a dynamic
CC assay range for that analyte. The method permits assays to be conducted
CC within their dynamic range without a need to dilute the reactants,
CC therefore, achieving a virtual dilution. The method permits measurement
CC of high concentration analytes in the same reaction mixture as low
CC concentration analytes therefore, reducing the number of separate
CC analyses necessary to complete a full clinical menu. The measurement does
CC not require problematic low-affinity receptors and does not significantly
CC affect other analyses in the reaction mixture. The current sequence
CC represents a leaving group peptide for use in a cellprobe reagent for
CC assaying enzyme activity.
XX

SQ Sequence 4 AA;
 Query Match 76.0%; Score 19; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
 DB 1 PRP 3

RESULT 30
 ADC15585
 ID ADC15585 standard; peptide; 4 AA.
 XX AC ADC15585;
 XX DT 18-DEC-2003 (first entry)
 XX DE Rho 110 labelled leaving group peptide #41.
 XX KW Assay; binding; target; analyte; enzyme activity.
 XX OS Synthetic.
 XX PN WO2003067212-A2.
 XX PD 14-AUG-2003.
 XX PF 21-JAN-2003; 2003WO-US001497.
 XX PR 08-FEB-2002; 2002US-00071395.
 XX PA (BECI) BECKMAN COULTER INC.
 XX PI Bell ML;
 XX DR WPI; 2003-689583/65.
 XX PT Assaying target analytes in a sample comprises determining the extent of binding between the target analyte and the solid support-bound ligand of the analyte useful for conducting multiplexed assays of multiple analytes.
 XX PS Disclosure; Page 33; 48pp; English.
 XX CC The invention relates to a method for assaying target analyte(s). The steric interference is provided by a solid support (s1). The method involves assaying target analyte(s) (A) in a sample comprising providing (A) and binding ligand (1) of (A) bound to a solid support, where the support is porous, the ligand is bound within the pores of the support ability, and the pores sterically interfere with the ability of the binding ligand to bind to (A) that does not hinder the binding of all other target analyte(s) to all other binding ligand(s). The method is efficiently capable of simultaneously assaying multiple different analytes and permits each target analyte to be assayed within a dynamic assay range for that analyte. The method permits assays to be conducted within their dynamic range without a need to dilute the reactants, therefore, achieving a virtual dilution. The method permits measurement of high concentration analytes in the same reaction mixture as low concentration analytes therefore, reducing the number of separate analyses necessary to complete a full clinical menu. The measurement does not require problematic low-affinity receptors and does not significantly affect other analyses in the reaction mixture. The current sequence represents a leaving group peptide for use in a cellprobe reagent for assaying enzyme activity.

SQ Sequence 4 AA;
 Query Match 76.0%; Score 19; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
 DB 1 PRP 3

RESULT 31
 ADC15559
 ID ADC15559 standard; peptide; 4 AA.
 XX AC ADC15559;
 XX DT 18-DEC-2003 (first entry)
 XX DE Rho 110 labelled leaving group peptide #15.
 XX KW Assay; binding; target; analyte; enzyme activity.
 XX OS Synthetic.
 XX PN WO2003067212-A2.
 XX PD 14-AUG-2003.
 XX PF 21-JAN-2003; 2003WO-US001497.
 XX PR 08-FEB-2002; 2002US-00071395.
 XX PA (BECI) BECKMAN COULTER INC.
 XX PI Bell ML;
 XX DR WPI; 2003-689583/65.
 XX PT Assaying target analytes in a sample comprises determining the extent of binding between the target analyte and the solid support-bound ligand of the analyte useful for conducting multiplexed assays of multiple analytes.
 XX PS Disclosure; Page 32; 48pp; English.
 XX CC The invention relates to a method for assaying target analyte(s). The steric interference is provided by a solid support (s1). The method involves assaying target analyte(s) (A) in a sample comprising providing (A) and binding ligand (1) of (A) bound to a solid support, where the support is porous, the ligand is bound within the pores of the support ability, and the pores sterically interfere with the ability of the binding ligand to bind to (A) that does not hinder the binding of all other target analyte(s) to all other binding ligand(s). The method is efficiently capable of simultaneously assaying multiple different analytes and permits each target analyte to be assayed within a dynamic assay range for that analyte. The method permits assays to be conducted within their dynamic range without a need to dilute the reactants, therefore, achieving a virtual dilution. The method permits measurement of high concentration analytes in the same reaction mixture as low concentration analytes therefore, reducing the number of separate analyses necessary to complete a full clinical menu. The measurement does not require problematic low-affinity receptors and does not significantly affect other analyses in the reaction mixture. The current sequence represents a leaving group peptide for use in a cellprobe reagent for assaying enzyme activity.

SQ Sequence 4 AA;
 Query Match 76.0%; Score 19; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
 DB 1 PRP 3

RESULT 32

ADDS2662
ID ADD52662 standard; peptide; 4 AA.
XX AC
XX ADD52662;
XX DT
XX 15-JAN-2004 (first entry)
XX DE
XX Angiogenesis inhibiting peptide seq id 12.
XX KW
XX antiangiogenic; cytostatic; immunosuppressive; antirheumatic;
XX antiarthritic; angiogenesis inhibitor; angiogenesis inhibitor; cancer;
XX autoimmune diseases; rheumatoid arthritis; immune arthritis;
XX degenerative arthritis.
XX OS
XX Synthetic.
XX FH
XX Key Modified-site Location/Qualifiers
FT FT /label= OTHER
FT FT /note= "OTHER= N-acetyl"
FT FT Modified-site 4
FT FT /label= OTHER
FT FT /note= "OTHER= Prolylethylamide"
XX XX
XX US2003109456-A1.
XX XX
XX 12-JUN-2003.
XX XX
XX 30-OCT-2002; 2002US-00283813.
XX XX
XX 31-OCT-2001; 2001US-0335018P.
XX XX
XX (HAVI/) HAVIV F.
XX (BRAD/) BRADLEY M F.
XX Havi F, Bradley MF;
XX WPI; 2003-829403/77.
XX DR
XX New compound useful for inhibiting angiogenesis or treating cancer in
XX mammal, or in prevention and treatment of other diseases such as
XX autoimmune diseases.
XX FT
XX Claim 9; SEQ ID NO 12; 21pp; English.
XX PS
XX The invention describes a tri-, tetra-, or pentapeptide compound (I). (I)
XX or a salt of it, is used in a pharmaceutical composition for inhibiting
XX angiogenesis or for treating cancer in a mammal. (I) can also be used for
XX the prevention or treatment of other diseases, such as autoimmune
XX diseases, e.g. rheumatoid, immune and degenerative arthritis. This is the
XX amino acid sequence of an angiogenesis inhibiting peptide.
XX CC
XX Sequence 4 AA;
SQ
Query Match 76.0%; Score 19; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 PRP 4
DB 2 PRP 4
RESULT 33
AAY80482
ID AAY80482 standard; peptide; 3 AA.
XX XX
XX AC AAY80482;
XX XX
XX 06-JUN-2000 (first entry)
XX DE
XX Cell adhesion peptide #17.
XX XX

KW Bone regenerative; osteopathic; osseous tissue; reconstitution;
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.
XX OS
XX Synthetic.
XX XX
XX WO200004941-A1.
XX FN
XX 03-FEB-2000.
XX PD
XX XX
XX 22-JUL-1999; 99WO-US016800.
XX PF
XX 24-JUL-1998; 98US-00122348.
XX PR
XX (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
XX PA
XX Budny JA;
XX PI
XX WPI; 2000-195084/17.
XX DR
XX System for reconstructing osseous tissue, useful e.g. for treating
FT fractures, comprises scaffold containing promoter of bone formation and
FT inhibitor of bone resorption.
XX FT
XX Claim 14; Page 31; 44pp; English.
XX PS
XX The invention relates to a novel system for reconstitution of osseous
CC tissue comprising a scaffold carrying a compound (I) that promotes bone
CC formation and a component that decreases bone resorption (II). (I)
CC induces migration and adhesion of osteoblasts and osteoclasts and (II)
CC inhibits proteolysis (specifically by plasmin) of extracellular matrix.
CC (I) is preferably selected from: selectin or selectin binding fragments,
CC proteins and peptides that facilitate cell adhesion, plasminogen
CC activator inhibitors, protease inhibitors and metalloprotease inhibitors.
CC The peptides AAY80466-Y80492 are claimed examples of cell adhesion
CC peptides used in the system of the invention. The system is used to
CC replace, remodel or correct bone defects, e.g. fractures, fissures or
CC bone mass loss. Incorporation of (I) into the scaffold results in rapid
CC seeding by osteoblasts and the development of an organic matrix, i.e. the
CC preformed scaffold replaces the rate-determining step of extracellular
CC matrix formation. The scaffold can be designed to have a predetermined
CC resorption/degradation rate, and may include regulatory compounds for
CC specific cell types
XX CC
XX Sequence 3 AA;
SQ
Query Match 72.0%; Score 18; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPR 3
DB 1 GPR 3
RESULT 34
AAB91977
ID AAB91977 standard; peptide; 3 AA.
XX XX
XX AC AAB91977;
XX XX
XX 22-JUN-2001 (first entry)
XX DT
XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1153.
XX DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX XX
XX Homo sapiens.
OS OS
OS Synthetic.
XX XX
XX WO200069900-A2.

XX PD 23-NOV-2000.
 XX PF 17-MAY-2000; 2000WO-US013576.
 XX PR 17-MAY-1999; 99US-0134406P.
 XX PR 10-SEP-1999; 99US-0153406P.
 XX PR 15-OCT-1999; 99US-0159783P.
 XX PA (CONJ-) CONJUCHEM INC.
 XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX PF WPI; 2001-112059/12.
 XX PR Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX PS Disclosure; Page 572; 733pp; English.
 XX CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX CC Sequence 3 AA;
 XX SQ
 Query Match 72.0%; Score 18; DB 4; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPR 3
 DB 1 GPR 3
 RESULT 35
 ABU60858
 ID ABU60858 standard; peptide; 3 AA.
 XX AC ABU60858;
 XX DT 06-MAY-2003 (first entry)
 XX DE Peptide production by gene recombination associated peptide #42.
 XX KW Peptide production; low-molecular peptide; KISS-1; GPR8 ligand;
 XX KW gene recombination.
 XX OS Synthetic.
 XX PN WO200292829-A1.
 XX PD 21-NOV-2002.
 XX PR 16-MAY-2002; 2002WO-JF004735.
 XX PR 17-MAY-2001; 2001JP-00147341.
 XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Nishimura O, Suenaga M, Ito T, Kitada C;
 XX PF WPI; 2003-129302/12.
 XX PR Process for producing peptides e.g. KISS-1 peptide and GPR8 ligand for
 PT subsequent applications by gene recombination technique through tandem
 PT repeats to provide precursor protein with specific cleavage sites.
 XX PS Claim 8; Page 42; 87pp; Japanese.
 XX CC The invention describes a method of producing a peptide comprising the
 CC excision of the N and C-terminals of a target peptide with enzymes or
 CC chemically through the attached cleavage sites repeated by ligation in a
 CC precursor protein. The method is for producing (low-molecular) peptides
 CC e.g. KISS-1 peptide and GPR8 ligand for subsequent applications by the
 CC gene recombination technique through tandem repeats to provide a
 CC precursor protein with specific cleavage sites. With this method, peptide
 CC production can be carried out easily to provide large quantities of the
 CC required peptides. This is the amino acid sequence of a peptide
 CC associated with the peptide production method of the invention
 XX SQ Sequence 3 AA;
 XX SQ Query Match 72.0%; Score 18; DB 6; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPR 3
 DB 1 GPR 3
 RESULT 36
 AAR26394
 ID AAR26394 standard; peptide; 4 AA.
 XX AC AAR26394;
 XX DT 25-MAR-2003 (revised)
 XX DT 25-JAN-1993 (first entry)
 XX DE Sequence of thrombus binding peptide.
 XX KW Technetium-99m labelled polypeptide imaging agent; radiolabeled imaging;
 XX KW radiodiagnostic agent.
 XX OS Synthetic.
 XX PN WO9213572-A1.
 XX PD 20-AUG-1992.
 XX PF 07-FEB-1992; 92WO-US0000757.
 XX PR 08-FEB-1991; 91US-00653012.
 XX PA (DIAT-) DIATECH INC.
 XX PI Dean RT;
 XX PF WPI; 1992-299767/36.
 XX PR New technetium-99m labelled polypeptide imaging agents - for imaging of
 PT clots, tumours, infection sites, atherosclerotic and amyloid plaques or
 PT bone, and for visualising organs.
 XX PS Claim 6; Page 13; 19pp; English.
 XX CC The binding peptide is covalently linked to a 'Cp(aa)Cp' technetium
 CC binding group wherein Cp is a protected cysteine and (aa) is an amino
 CC acid. The technetium-99m complexes are used to image target sites within
 CC a mammalian body. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4 AA;
Query Match 72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 37
AAR32383
ID AAR32383 standard; peptide; 4 AA.
XX AC AAR32383;
XX DT 25-MAR-2003 (revised)
DT 01-JUL-1993 (first entry)
XX DE Fibrinogen binding peptide #7.
XX KW platelet aggregation; fibrinogen A-alpha chain; protein scrambling;
KW GPR-like peptide.
XX OS Synthetic.
XX PN WO9304079-A1.
XX PD 04-MAR-1993.
XX PF 20-AUG-1992; 92WO-US006933.
XX PR 21-AUG-1991; 91US-00813315.
PA (RECE-) RECEPTOR LAB INC.
PI Venton DL, Hopfinger AJ, Le Breton G;
XX MPI; 1993-093932/11.
XX Identifying peptide(s) which bond to predetermined targets - by random
PT degradation and recombination of peptide(s) and isolating bound
peptide(s).
XX OS Synthetic.
XX PN WO9304079-A1.
XX PD 04-MAR-1993.
XX PF 20-AUG-1992; 92WO-US006933.
XX PR 21-AUG-1991; 91US-00813315.
PA (RECE-) RECEPTOR LAB INC.
PI Venton DL, Hopfinger AJ, Le Breton G;
XX MPI; 1993-093932/11.
XX Identifying peptide(s) which bond to predetermined targets - by random
PT degradation and recombination of peptide(s) and isolating bound
peptide(s).

PS Example 5; Page 58; 89pp; English.

XX SQ Sequence 4 AA;
Query Match 72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 38
AAR32384
ID AAR32384 standard; peptide; 4 AA.
XX AC AAR32384;
XX DT 25-MAR-2003 (revised)

XX SQ Sequence 4 AA;
Query Match 72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 39
AAR32385
ID AAR32385 standard; peptide; 4 AA.
XX AC AAR32385;
XX DT 25-MAR-2003 (revised)
DT 01-JUL-1993 (first entry)
XX DE Fibrinogen binding peptide generated by scrambling.
XX KW Fibrinogen binding peptide generated by scrambling;
KW platelet aggregation; fibrinogen A-alpha chain; protein scrambling;
KW GPR-like peptide.
XX OS Synthetic.
XX PN WO9304079-A1.
XX PD 04-MAR-1993.
XX PF 20-AUG-1992; 92WO-US006933.
XX PR 21-AUG-1991; 91US-00813315.

CC recognition site for a chemical cleavage reagent as well as one for an
 CC enzymatic cleavage reagent. The multicopy fusion protein is used to
 CC produce single copies of GPR modified at the N-terminal with a
 CC pyroglutanyl residue and modified at the C-terminal by amidation.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

Query Match

Best Local Similarity 72.0%; Score 18; DB 2; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3

Db 2 GPR 4

RESULT 42

AAR49797

ID AAR49797 standard; peptide; 4 AA.

XX AAR49797;

XX 25-MAR-2003 (revised)

DT 23-AUG-1994 (first entry)

XX

DE Sequence of peptide which binds to human fibrinogen.

XX Random degradation; recombination; scrambling reaction.

KW

OS Synthetic.

XX

XX WO9404558-A1.

XX 03-MAR-1994.

PD

XX 09-AUG-1993; 93WO-US008231.

XX 21-AUG-1992; 92US-00932200.

PR

XX (RECE-) RECEPTOR LAB INC.

XX

XX Venton DL, Hopfinger AJ;

PI

XX WPI; 1994-083103/10.

DR

XX Identifying peptides which binds to a specific target - by contacting
 PT target with scrambled equilibrium mixt. of many peptide derived from
 PT protein by incubation with protease, for detecting potential therapeutic
 PT agents.

PS

XX Example; Page 54; 97pp; English.

XX The inventors claim a method for inexpensively and rapidly producing a
 CC large and varied population of peptides and screening this varied
 CC population for the presence of peptides which bind to a target, for
 CC example, a macromolecule associated with a particular physiological
 CC function. The specific binding peptides are isolated and sequenced,
 CC synthesised on a large-scale, their biological activity is demonstrated,
 CC and then subjected to clinical testing. The random population of peptides
 CC is generated by employing a scrambling system which utilises one or more
 CC chymotrypsin, subtilisin and dipeptidyl peptidase IV. A typical starting
 CC protein is casein. Targets are esp. receptors involved in physiological
 CC processes, partic. fibrinogen; sickle cell haemoglobin; collagenase IV;
 CC rennin; Gp. IIb IIIa or phospholipase A2. It has been demonstrated that
 CC synthetic peptides beginning with the sequence GPR will bind to
 CC fibrinogen. Such peptides include GPR, GPRP and GPRV. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

SQ Sequence 4 AA;

Query Match

Best Local Similarity 72.0%; Score 18; DB 2; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3

Db 1 GPR 3

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3

Db 1 GPR 3

RESULT 43

AAR49798

ID AAR49798 standard; peptide; 4 AA.

XX AAR49798;

XX 25-MAR-2003 (revised)

DT 23-AUG-1994 (first entry)

XX

DE Sequence of peptide which binds to human fibrinogen.

XX Random degradation; recombination; scrambling reaction.

XX

OS Synthetic.

XX

XX WO9404558-A1.

XX 03-MAR-1994.

PD

XX 09-AUG-1993; 93WO-US008231.

XX

XX 21-AUG-1992; 92US-00932200.

PR

XX (RECE-) RECEPTOR LAB INC.

XX

XX Venton DL, Hopfinger AJ;

PI

XX WPI; 1994-083103/10.

DR

XX Identifying peptides which binds to a specific target - by contacting
 PT target with scrambled equilibrium mixt. of many peptide derived from
 PT protein by incubation with protease, for detecting potential therapeutic
 PT agents.

PS

XX Example; Page 54; 97pp; English.

XX The inventors claim a method for inexpensively and rapidly producing a
 CC large and varied population of peptides and screening this varied
 CC population for the presence of peptides which bind to a target, for
 CC example, a macromolecule associated with a particular physiological
 CC function. The specific binding peptides are isolated and sequenced,
 CC synthesised on a large-scale, their biological activity is demonstrated,
 CC and then subjected to clinical testing. The random population of peptides
 CC is generated by employing a scrambling system which utilises one or more
 CC proteases, esp. papain, pepsin, bromelain, thermolysin, trypsin, pronase,
 CC chymotrypsin, subtilisin and dipeptidyl peptidase IV. A typical starting
 CC protein is casein. Targets are esp. receptors involved in physiological
 CC processes, partic. fibrinogen; sickle cell haemoglobin; collagenase IV;
 CC rennin; Gp. IIb IIIa or phospholipase A2. It has been demonstrated that
 CC synthetic peptides beginning with the sequence GPR will bind to
 CC fibrinogen. Such peptides include GPR, GPRP and GPRV. HPLC fractions
 CC bound to fibrinogen were screened on CE. Three of these GPR peaks were
 CC collected and sequenced and found to be GPRL, GPRF and LPRK. In addition,
 CC a GPR-independent peak was also collected and found to have the sequence
 CC DKPDNF. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 4 AA;

Query Match

Best Local Similarity 72.0%; Score 18; DB 2; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3

Db 1 GPR 3

AC AAR60327;
 XX
 DT 07-MAR-1995 (first entry)
 XX Blood coagulation inhibiting peptide.
 DE Blood; fibrin; coagulation; inhibition; thrombin; fibrinogen.
 XX
 XX Synthetic.
 OS
 XX JP06179696-A.
 PN
 XX 28-JUN-1994.
 PD
 XX 19-MAR-1993; 93JP-00085678.
 PF
 XX 13-OCT-1992; 92JP-00300380.
 PR
 XX (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 XX (NIHA-) NIPPON HAM KK.
 PA
 XX WPI; 1994-245692/30.
 DR
 XX New blood coagulation inhibiting peptide(s) having fibrin-agglutination
 PT inhibitory activity - useful for the treatment and prevention of
 PT thrombosis.
 XX
 PS Claim 1; Page 2; 6pp; Japanese.
 XX
 CC The blood coagulation inhibiting peptide comprises L-form amino acids and
 CC has fibrin agglutination inhibiting activity. Such peptides (see AAR60327
 CC -R60335) were synthesised using a peptide synthesiser (Applied Biosystems
 CC Co.; 430A) and purified by high pressure liquid chromatography. To 0.2 ml
 CC of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was
 CC added and incubated for 1 minute at 37 deg. Celsius. 0.2 ml of thrombin
 CC solution was added and the IC50 was determined according to the method of
 CC Kawasaki et al. This peptide had an IC50 of 510 micromolar compared with
 CC a control peptide of Gly-Pro-Arg which registered an IC50 of 250
 CC micromolar.
 CC
 SQ Sequence 4 AA;
 Query Match 72.0%; Score 18; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPR 3
 DB 1 GPR 3
 RESULT 46
 AAR09862
 ID AAR09862 standard; peptide; 4 AA.
 XX
 XX AAR09862;
 AC
 XX 30-JUN-1997 (first entry)
 DT
 XX Thrombin inhibitor.
 DE
 XX Thrombin; inhibitor; aggregation; platelet; determination; assay;
 KW qualitative; quantitative; fibrin.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 4 /note= "MeGly"
 FT
 XX EP661383-A2.
 PN
 XX 05-JUL-1995.
 PD

RESULT 44
 AAR49799
 ID AAR49799 standard; peptide; 4 AA.
 XX
 AC AAR49799;
 XX
 XX 25-MAR-2003 (revised)
 DT 23-AUG-1994 (first entry)
 XX
 XX Sequence of peptide which binds to human fibrinogen.
 DE
 XX Random degradation; recombination; scrambling reaction.
 KW
 XX Synthetic.
 OS
 XX WO9404558-A1.
 PN
 XX 03-MAR-1994.
 PD
 XX 09-AUG-1993; 93WO-US008231.
 PF
 XX 21-AUG-1992; 92US-00932200.
 PR
 XX (RECE-) RECEPTOR LAB INC.
 PA
 XX Venton DL, Hopfinger AJ;
 PI
 XX WPI; 1994-083103/10.
 DR
 XX Identifying peptides which binds to a specific target - by contacting
 PT target with scrambled equilibrium mixt. of many peptide derived from
 PT protein by incubation with protease, for detecting potential therapeutic
 PT agents.
 XX
 PS Example; Page 54; 97pp; English.
 XX
 CC The inventors claim a method for inexpensively and rapidly producing a
 CC large and varied population of peptides and screening this varied
 CC population for the presence of peptides which bind to a target, for
 CC example, a macromolecule associated with a particular physiological
 CC function. The specific binding peptides are isolated and sequenced.
 CC synthesised on a large-scale, their biological activity is demonstrated,
 CC and then subjected to clinical testing. The random population of peptides
 CC is generated by employing a scrambling system which utilises one or more
 CC proteases, esp. papain, pepsin, bromelain, thermolysin, trypsin, pronase,
 CC chymotrypsin, subtilisin and dipeptidyl peptidase IV. A typical starting
 CC protein is casein. Targets are esp. receptors involved in physiological
 CC processes, partic. fibrinogen; sickle cell haemoglobin; collagenase IV;
 CC rennin; Gp. IIb IIIa or phospholipase A2. It has been demonstrated that
 CC synthetic peptides beginning with the sequence GPR will bind to
 CC fibrinogen. Such peptides include GPR, GPRP and GPRV. HPLC fractions
 CC bound to fibrinogen were screened on CB. Three of these GPR peaks were
 CC collected and sequenced and found to be GPRLL, GPRF and LPK. In addition,
 CC a GPR-independent peak was also collected and found to have the sequence
 CC DKPDNF. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;
 Query Match 72.0%; Score 18; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPR 3
 DB 1 GPR 3
 RESULT 45
 AAR60327
 ID AAR60327 standard; peptide; 4 AA.
 XX

XX PF 15-DEC-1994; 94EP-00119803.
 XX PR 30-DEC-1993; 93DE-04344919.
 XX PA (BSHW) BEHRINGER AG.
 XX PI Reers M;
 XX DR WPI; 1995-233339/31.
 XX PT Determn. of thrombin-induced platelet aggregation in presence of fibrin -
 PT comprises use of fibrin aggregation inhibitor to suppress fibrin clot
 PT formation.
 XX PS Claim 5; Col 6; 5pp; German.
 XX CC In the qualitative or quantitative determn. of thrombin-induced platelet
 CC aggregation in the presence of fibrin, interference from fibrin clot
 CC formation is suppressed with a fibrin-aggregation inhibitor (e.g.
 CC AAW09861-63). The assay may be used to determine the platelet aggregation
 CC inhibitory activity of thrombin inhibitors. The peptides inhibit fibrin
 CC clot formation at high thrombin concns. without inhibiting platelet
 CC aggregation
 XX SQ Sequence 4 AA;
 Query Match 72.0%; Score 18; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPR 3
 DB 1 GPR 3
 RESULT 47
 AAR80052 72.0%; Score 18; DB 2; Length 4;
 ID AAR80052 standard; peptide; 4 AA.
 XX AC AAR80052;
 XX DT 25-APR-1996 (first entry)
 XX DE Peptidase substrate #6.
 XX KW Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
 XX cerebral function.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "sarcosine (N-methylglycine)"
 XX JPO7227281-A.
 XX PD 29-AUG-1995.
 XX PF 15-FEB-1994; 94JP-00042027.
 XX PR 15-FEB-1994; 94JP-00042027.
 XX PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 XX PA (NIHA-) NIPPON HAM KK.
 XX XX WPI; 1995-331519/43.
 XX DR 140 kDa peptidase hydrolyses proline rich proteins - useful for
 XX PT prevention and treatment of diseases related to proline rich proteins and
 XX PT studies of cerebral functions.
 XX PS Example 4; Page 6; 7pp; Japanese.
 XX CC The sequences represented by AAR80045 and AAR80048-R80059 are substrates
 CC for the novel peptidase of the invention. The peptidase hydrolyses P-P-P-
 CC P, P-P-P, and P-P and recognises the proline at the second residue from
 CC the N-terminal of a peptide to release the N-terminal amino acid. The
 CC enzyme's activity is stimulated with MnCl2 and inhibited with o-
 CC phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
 CC hydrolysis of proline containing physiologically active peptides,
 CC oligoproline and proline rich proteins in the living body, particularly
 CC in the brain of mammals. The peptidase is useful for the prevention and
 CC treatment of proline rich protein related diseases and study of cerebral
 CC functions
 XX SQ Sequence 4 AA;

CC the N-terminal of a peptide to release the N-terminal amino acid. The
 CC enzyme's activity is stimulated with MnCl2 and inhibited with o-
 CC phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
 CC hydrolysis of proline containing physiologically active peptides,
 CC oligoproline and proline rich proteins in the living body, particularly
 CC in the brain of mammals. The peptidase is useful for the prevention and
 CC treatment of proline rich protein related diseases and study of cerebral
 CC functions
 XX SQ Sequence 4 AA;
 Query Match 72.0%; Score 18; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 48
 AAR80053
 ID AAR80053 standard; peptide; 4 AA.
 XX AC AAR80053;
 XX DT 25-APR-1996 (first entry)
 XX DE Peptidase substrate #7.
 XX KW Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
 XX cerebral function.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "sarcosine (N-methylglycine)"
 XX JPO7227281-A.
 XX PD 29-AUG-1995.
 XX PF 15-FEB-1994; 94JP-00042027.
 XX PR 15-FEB-1994; 94JP-00042027.
 XX PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 XX PA (NIHA-) NIPPON HAM KK.
 XX XX WPI; 1995-331519/43.
 XX DR 140 kDa peptidase hydrolyses proline rich proteins - useful for
 XX PT prevention and treatment of diseases related to proline rich proteins and
 XX PT studies of cerebral functions.
 XX PS Example 4; Page 6; 7pp; Japanese.
 XX CC The sequences represented by AAR80046 and AAR80048-R80059 are substrates
 CC for the novel peptidase of the invention. The peptidase hydrolyses P-P-P-
 CC P, P-P-P, and P-P and recognises the proline at the second residue from
 CC the N-terminal of a peptide to release the N-terminal amino acid. The
 CC enzyme's activity is stimulated with MnCl2 and inhibited with o-
 CC phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
 CC hydrolysis of proline containing physiologically active peptides,
 CC oligoproline and proline rich proteins in the living body, particularly
 CC in the brain of mammals. The peptidase is useful for the prevention and
 CC treatment of proline rich protein related diseases and study of cerebral
 CC functions
 XX SQ Sequence 4 AA;

Query Match 72.0%; Score 18; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
 |||
 Db 1 GPPP 4

RESULT 49
 AAR69071
 ID AAR69071 standard; peptide; 4 AA.
 XX
 AC AAR69071;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-OCT-1995 (first entry)
 XX
 DE Interconnecting peptide for the fusion protein construct GRF 1-41.
 XX
 KW Growth Hormone Releasing Factor 1; GRF 1; endopeptidase; thrombin;
 KW cleavage; interconnecting peptide.
 XX
 OS Synthetic.
 XX
 PN WO9503405-A2.
 XX
 PD 02-FEB-1995.
 XX
 PF 19-JUL-1994; 94WO-US008125.
 XX
 PR 20-JUL-1993; 93US-00095162.
 XX
 PA (BION-) BIONEERASKA INC.
 XX
 PI Wagner FW, Stout J, Henriksen D, Partridge B, Manning S;
 XX
 DR WPI; 1995-075233/10.
 XX
 PT Transpeptidation of recombinant polypeptides - using endopeptidase such
 PT as trypsin or thrombin to modify C-terminal residue.
 XX
 PS Disclosure; Page 23; 69pp; English.
 XX
 CC The example concerns the transpeptidation of a single copy recombinant
 CC polypeptide derived from a fusion protein construct. The binding protein
 CC of the fusion protein construct will be connected to the single copy
 CC recombinant polypeptide through an interconnecting peptide. For example,
 CC the tetrapeptide AAR69071 is a suitable interconnecting peptide for the
 CC fusion protein construct contg. the GRF (1-41)-Ala-Arg-Leu-Ala single
 CC copy recombinant polypeptide. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 4 AA;

Query Match 72.0%; Score 18; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
 |||
 Db 2 GPR 4

RESULT 50
 AAW11088
 ID AAW11088 standard; peptide; 4 AA.
 XX
 AC AAW11088;
 XX
 DT 03-JUN-1997 (first entry)
 XX
 DE Thrombus-targeting peptide used in diagnostic imaging.

XX Leukocyte; target; direct; chelator; radionuclide; radiolabel; isotope;
 KW atherosclerosis; thrombosis; embolism; infection; thrombus; diagnosis;
 KW imaging.
 XX
 OS Synthetic.
 XX
 PN WO9603427-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 28-APR-1995; 95WO-CA000249.
 XX
 PR 22-JUL-1994; 94US-00279155.
 XX
 XX (RESO-) RESOLUTION PHARM INC.
 XX
 PA Pollak A, Goodbody A;
 XX
 DR WPI; 1996-116994/12.
 XX
 PT New peptide derived radionuclide chelators and metal complexes - useful
 PT for diagnostic imaging.
 XX
 PS Disclosure; Page 7; 30pp; English.
 XX
 CC AAW11087-W11089 are peptides used for targeting agents to a thrombus.
 CC The peptides may be coupled to a chelator molecule, which is labelled
 CC with a diagnostically useful metal nuclide to form a peptide derived
 CC radionuclide chelator molecules. Such targeted and labelled chelators
 CC are used to detect pathological conditions by diagnostic imaging.
 CC Radionuclides used include 99mTc, 64Cu, 67Cu, 108Rh, 103Pd, 186Re,
 CC 188Re, 198Au, 199Au, 203Pb, 212Pb and 212Bi. The coupling of a targeting
 CC agent and radionuclide using a chelating agent is an alternative to the
 CC direct labelling of targeting agents in which radionuclides are typically
 CC bound at the more numerous low-affinity sites, forming unstable
 CC complexes. The new conjugates give better scintigraphic images in rat
 CC inflammation studies than known imaging agents Ga-67, 99mTc-IGG, 111In-
 CC WBC and 99mTc-Nanocol. They image more rapidly than the known agents and
 CC show superior biodistribution
 XX
 SQ Sequence 4 AA;

Query Match 72.0%; Score 18; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
 |||
 Db 1 GPR 3

Search completed: September 7, 2004, 19:24:22
 Job time : 54 secs

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OM protein - protein search, using sw model

Run on: September 7, 2004, 18:54:02 ; Search time 31 Seconds
(without alignments)

6.661 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	25	100.0	4	1	US-07-934-553-5	Sequence 5, Appli
2	25	100.0	4	1	US-07-932-200-6	Sequence 6, Appli
3	25	100.0	4	1	US-08-022-381A-1	Sequence 1, Appli
4	25	100.0	4	1	US-08-225-474-5	Sequence 5, Appli
5	25	100.0	4	1	US-08-365-759-2	Sequence 2, Appli
6	25	100.0	4	1	US-08-475-827A-1	Sequence 1, Appli
7	25	100.0	4	2	US-08-387-749-6	Sequence 6, Appli
8	25	100.0	4	2	US-08-747-137-81	Sequence 81, Appli
9	25	100.0	4	2	US-08-753-781-2	Sequence 2, Appli
10	25	100.0	4	3	US-08-993-185-6	Sequence 6, Appli
11	25	100.0	4	3	US-08-611-395-5	Sequence 5, Appli
12	25	100.0	4	4	US-09-540-448-6	Sequence 6, Appli
13	25	100.0	4	4	US-09-243-640-4	Sequence 4, Appli
14	25	100.0	4	4	US-08-929-847-6	Sequence 6, Appli
15	25	100.0	4	5	PCT-US93-08231-6	Sequence 6, Appli
16	25	100.0	4	5	PCT-US95-07542-4	Sequence 4, Appli
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18	25	100.0	5	1	US-08-022-381A-3	Sequence 3, Appli
19	25	100.0	5	1	US-08-022-381A-4	Sequence 4, Appli
20	25	100.0	5	1	US-08-022-381A-5	Sequence 5, Appli
21	25	100.0	5	1	US-08-022-381A-6	Sequence 6, Appli
22	25	100.0	5	1	US-08-022-381A-7	Sequence 7, Appli
23	25	100.0	5	1	US-08-022-381A-8	Sequence 8, Appli
24	25	100.0	5	1	US-08-022-381A-9	Sequence 9, Appli
25	25	100.0	5	1	US-08-022-381A-10	Sequence 10, Appli
26	25	100.0	5	1	US-08-022-381A-11	Sequence 11, Appli
27	25	100.0	5	1	US-08-022-381A-12	Sequence 12, Appli

28	25	100.0	5	1	US-08-022-381A-13	Sequence 13, Appli
29	25	100.0	5	1	US-08-022-381A-14	Sequence 14, Appli
30	25	100.0	5	1	US-08-022-381A-15	Sequence 15, Appli
31	25	100.0	5	1	US-08-475-827A-2	Sequence 2, Appli
32	25	100.0	5	1	US-08-475-827A-3	Sequence 3, Appli
33	25	100.0	5	1	US-08-475-827A-4	Sequence 4, Appli
34	25	100.0	5	1	US-08-475-827A-5	Sequence 5, Appli
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41	25	100.0	5	1	US-08-475-827A-12	Sequence 12, Appli
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43	25	100.0	5	1	US-08-475-827A-14	Sequence 14, Appli
44	25	100.0	5	1	US-08-475-827A-15	Sequence 15, Appli
45	25	100.0	5	1	US-08-595-718A-4	Sequence 4, Appli
46	25	100.0	5	1	US-08-672-255-1	Sequence 1, Appli
47	25	100.0	6	1	US-08-022-381A-16	Sequence 16, Appli
48	25	100.0	6	1	US-08-022-381A-17	Sequence 17, Appli
49	25	100.0	6	1	US-08-022-381A-18	Sequence 18, Appli
50	25	100.0	6	1	US-08-022-381A-19	Sequence 19, Appli
51	25	100.0	6	1	US-08-022-381A-20	Sequence 20, Appli
52	25	100.0	6	1	US-08-022-381A-21	Sequence 21, Appli
53	25	100.0	6	1	US-08-365-759-3	Sequence 3, Appli
54	25	100.0	6	1	US-08-475-827A-16	Sequence 16, Appli
55	25	100.0	6	1	US-08-475-827A-17	Sequence 17, Appli
56	25	100.0	6	1	US-08-475-827A-18	Sequence 18, Appli
57	25	100.0	6	1	US-08-475-827A-19	Sequence 19, Appli
58	25	100.0	6	1	US-08-475-827A-20	Sequence 20, Appli
59	25	100.0	6	1	US-08-475-827A-21	Sequence 21, Appli
60	25	100.0	8	1	US-08-482-880-33	Sequence 33, Appli
61	25	100.0	8	2	US-08-273-274-33	Sequence 33, Appli
62	25	100.0	8	2	US-08-475-041-33	Sequence 33, Appli
63	25	100.0	8	2	US-08-484-773-33	Sequence 33, Appli
64	25	100.0	8	3	US-08-882-046-105	Sequence 105, Appli
65	25	100.0	9	4	US-09-721-870-86	Sequence 86, Appli

ALIGNMENTS

RESULT 1
US-07-934-553-5
Sequence 5, Application US/07934553
Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING Ige
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLON, LUNGWUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:

NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-5

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 2
US-07-932-200-6
Sequence 6, Application US/07932200
Patent No. 536862

GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: LE BRETON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FILING DATE: 21-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-932-200-6

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

Db 1 GPRP 4

RESULT 3

US-08-022-381A-1
Sequence 1, Application US/08022381A
Patent No. 547810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: -08-MAY-1990

ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-022-381A-1

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 4

US-08-225-474-5
Sequence 5, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: Patterson, Roy

APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: IGE Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut


```

; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,474
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU 9033-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-225-474-5

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 5
US-08-365-759-2
; Sequence 2, Application US/08365759
; Patent No. 5563041
; GENERAL INFORMATION:
; APPLICANT: Reers, Martin
; TITLE OF INVENTION: Method for Determining Platelet
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,759
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Toohy, Kimberlin M.

; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,474
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU 9033-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-225-474-5

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 6
US-08-475-827A-1
; Sequence 1, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; US-08-475-827A-1
Query Match      100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 7
US-08-387-749-6
; Sequence 6, Application US/08387749
; Patent No. 5814460
; GENERAL INFORMATION:
; APPLICANT: VENTON, DUANE L.
; APPLICANT: HOPFINGER, ANTON J.
; APPLICANT: LE BRETON, GUY
; TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
; TITLE OF INVENTION: USEFUL PEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,749
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08231
; FILING DATE: 09-AUG-1993
; PRIOR APPLICATION DATA: US 07/932,200
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,315
; FILING DATE: 21-AUG-1991
; PRIOR APPLICATION DATA: PCT/US91/00891
; FILING DATE: 14-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/480,865
; FILING DATE: 14-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: VENTON-1C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-387-749-6

Query Match      100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 8
US-08-747-137-81
; Sequence 81, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
US-08-747-137-81

Query Match      100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 9
US-08-753-781-2
; Sequence 2, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
US-08-753-781-2

Query Match      100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Eladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DITI 124
; CURRENT APPLICATION NUMBER: US/08/753.781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-753-781-2

Query Match      100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
Db      1 GPRP 4

RESULT 10
US-08-993-165-6
; Sequence 6, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yundiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993.165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
US-08-993-165-6

Query Match      100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
Db      1 GPRP 4

RESULT 11
US-08-611-395-5
; Sequence 5, Application US/08611395
; Patent No. 6168939
; GENERAL INFORMATION:
; APPLICANT: SASAKI, MASAAHIRO
; APPLICANT: BOSMAN, BOUKJE
; APPLICANT: TAN, PARIS S. T.
; APPLICANT: TAKAFUJI, SHIN/ICHI
; APPLICANT: IWASAKI, TAISUKE
; TITLE OF INVENTION: NOVEL ENDOPEPTIDASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
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; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611.395
; FILING DATE: 06-Mar-1996
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-611-395-5

Query Match      100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
Db      1 GPRP 4

RESULT 12
US-09-540-448-6
; Sequence 6, Application US/99540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/09/540.448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
US-09-540-448-6

Query Match      100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
Db      1 GPRP 4

RESULT 13
US-09-243-640-4
; Sequence 4, Application US/09243640
; Patent No. 6521211
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;/ GENERAL INFORMATION:
;/ APPLICANT: Unger, Evan C
;/ APPLICANT: Shen, Dekang
;/ APPLICANT: Wu, Guanli
;/ TITLE OF INVENTION: No. 6521211el Methods Of Imaging And Treatment With Targeted
;/ TITLE OF INVENTION: Compositions
;/ FILE REFERENCE: DUP-0463
;/ CURRENT APPLICATION NUMBER: US/09/243,640
;/ CURRENT FILING DATE: 1999-02-03
;/ PRIOR APPLICATION NUMBER: 08/660,032
;/ PRIOR FILING DATE: 1996-06-06
;/ PRIOR APPLICATION NUMBER: 08/640,464
;/ PRIOR FILING DATE: 1996-05-01
;/ PRIOR APPLICATION NUMBER: 08/497,684
;/ PRIOR FILING DATE: 1995-06-07
;/ PRIOR APPLICATION NUMBER: 09/218,660
;/ PRIOR FILING DATE: 1998-12-22
;/ PRIOR APPLICATION NUMBER: 60/073,913
;/ PRIOR FILING DATE: 1998-02-06
;/ NUMBER OF SEQ ID NOS: 22
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 4
;/ LENGTH: 4
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
US-09-243-640-4

Query Match 100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 14
US-08-929-847-6
;/ Sequence 6, Application US/08929847
;/ Patent No. 6548047
;/ GENERAL INFORMATION:
;/ APPLICANT: Unger, Evan C.
;/ TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
;/ FILE REFERENCE: BMS0441
;/ CURRENT APPLICATION NUMBER: US/08/929,847
;/ CURRENT FILING DATE: 1997-09-15
;/ NUMBER OF SEQ ID NOS: 39
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 6
;/ LENGTH: 4
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-6

Query Match 100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 15
PCT-US93-08231-6
;/ Sequence 6, Application PC/TUS9308231
;/ GENERAL INFORMATION:
;/ APPLICANT: VENTON, DUANE L.
;/ APPLICANT: HOPFINGER, ANTON J.

;/ APPLICANT: LE BRETON, GUY
;/ TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
;/ TITLE OF INVENTION: USEFUL PEPTIDES
;/ NUMBER OF SEQUENCES: 20
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: BROWDY AND NEIMARK
;/ STREET: 419 SEVENTH STREET, N.W.
;/ CITY: WASHINGTON
;/ STATE: D.C.
;/ COUNTRY: U.S.A.
;/ ZIP: 20004
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US93/08231
;/ FILING DATE:
;/ CLASSIFICATION:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: COOPER, IVER P.
;/ REGISTRATION NUMBER: 28,005
;/ REFERENCE/DOCKET NUMBER: VENTONLC.PCT
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-628-5197
;/ TELEFAX: 202-737-3528
;/ TELEX: 248633
;/ INFORMATION FOR SEQ ID NO: 6:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 4 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
PCT-US93-08231-6

Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 16
PCT-US95-07542-4
;/ Sequence 4, Application PC/TUS9507542
;/ GENERAL INFORMATION:
;/ APPLICANT:
;/ TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
;/ TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS
;/ NUMBER OF SEQUENCES: 20
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US95/07542
;/ FILING DATE: 13-JUN-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/260,514
;/ FILING DATE: 15-JUN-1994
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 4 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ HYPOTHETICAL: NO
;/ FRAGMENT TYPE: internal

ORIGINAL SOURCE:
ORGANISM: Ligand sequence recognized by integrin
PC-US95-07542-4

Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 17
US-08-022-381A-2
Sequence 2, Application US/08022381A
Patent No. 5478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
TITLE OF INVENTION: Peptide Amides, Processes for the
Preparation Thereof and Agents Containing These as
Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunne
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022.381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-022-381A-2

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 18
US-08-022-381A-3

Sequence 3, Application US/08022381A
Patent No. 5478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
TITLE OF INVENTION: Peptide Amides, Processes for the
Preparation Thereof and Agents Containing These as
Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunne
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022.381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-022-381A-3

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 19
US-08-022-381A-4
Sequence 4, Application US/08022381A
Patent No. 5478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
TITLE OF INVENTION: Peptide Amides, Processes for the
Preparation Thereof and Agents Containing These as
Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunne
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: DC

```
/
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 24-FEB-1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION NUMBER: US 07/696,085
/ FILING DATE: 06-MAY-1991
/ APPLICATION NUMBER: DE 40 14 655.3
/ FILING DATE: 08-MAY-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Markowicz, Karen R.
/ REGISTRATION NUMBER: 36,351
/ REFERENCE/DOCKET NUMBER: 05552.1054-01000
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-022-381A-5

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
Db 1 GRRP 4

RESULT 21
US-08-022-381A-6
/ Sequence 6, Application US/08022381A
/ Patent No. 5478810
/ GENERAL INFORMATION:
/ APPLICANT: Stuber, Werner
/ APPLICANT: Fickenscher, Karl
/ TITLE OF INVENTION: Peptide Amides, Processes for the
/ TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
/ TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESSEE: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/022,381A
/ FILING DATE: 24-FEB-1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/696,085
/ FILING DATE: 06-MAY-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE 40 14 655.3
/ FILING DATE: 08-MAY-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Markowicz, Karen R.
/ REGISTRATION NUMBER: 36,351
/ REFERENCE/DOCKET NUMBER: 05552.1054-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/

/
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 24-FEB-1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION NUMBER: US 07/696,085
/ FILING DATE: 06-MAY-1991
/ APPLICATION NUMBER: DE 40 14 655.3
/ FILING DATE: 08-MAY-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Markowicz, Karen R.
/ REGISTRATION NUMBER: 36,351
/ REFERENCE/DOCKET NUMBER: 05552.1054-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-022-381A-5

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
Db 1 GRRP 4

RESULT 20
US-08-022-381A-5
/ Sequence 5, Application US/08022381A
/ Patent No. 5478810
/ GENERAL INFORMATION:
/ APPLICANT: Stuber, Werner
/ APPLICANT: Fickenscher, Karl
/ TITLE OF INVENTION: Peptide Amides, Processes for the
/ TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
/ TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESSEE: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/022,381A
/ FILING DATE: 24-FEB-1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/696,085
/ FILING DATE: 06-MAY-1991
/ PRIOR APPLICATION DATA:
```

US-08-022-381A-6

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 1 GPRP 4

RESULT 22

US-08-022-381A-7
; Sequence 7, Application US/08022381A
; Patent No. 5478910

; GENERAL INFORMATION:

; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes for the
; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,381A
; FILING DATE: 24-FEB-1993
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Matkiewicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 05552.1054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO:

7:

; SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-022-381A-7

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 1 GPRP 4

RESULT 23

US-08-022-381A-8
; Sequence 8, Application US/08022381A
; Patent No. 5478810

; GENERAL INFORMATION:

; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes for the
; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,381A
; FILING DATE: 24-FEB-1993
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Matkiewicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 05552.1054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO:

8:

; SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-022-381A-8

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 1 GPRP 4

RESULT 24

US-08-022-381A-9
; Sequence 9, Application US/08022381A
; Patent No. 5478810

; GENERAL INFORMATION:

; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes for the
; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-022-381A-9

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 25
US-08-022-381A-10
Sequence 10, Application US/08022381A
Patent No. 5478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
PREPARATION THEREOF AND AGENTS CONTAINING THESE AS
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-022-381A-11

ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-022-381A-10

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 26
US-08-022-381A-11
Sequence 11, Application US/08022381A
Patent No. 5478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
PREPARATION THEREOF AND AGENTS CONTAINING THESE AS
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 05552.1054-01000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-022-381A-11

Query Match 100.0%; Score 25; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 27
 US-08-022-381A-12
 ; Sequence 12, Application US/08022381A
 ; Patent No. 5478810
 ; GENERAL INFORMATION:
 ; APPLICANT: Stuber, Werner
 ; TITLE OF INVENTION: Peptide Amides, Processes for the
 ; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
 ; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/022,381A
 ; FILING DATE: 24-FEB-1993
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/696,085
 ; FILING DATE: 06-MAY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 40 14 655.3
 ; FILING DATE: 08-MAY-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Markowicz, Karen R.
 ; REGISTRATION NUMBER: 36,351
 ; REFERENCE/DOCKET NUMBER: 05552.1054-01000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-022-381A-12

Query Match 100.0%; Score 25; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 28
 US-08-022-381A-13
 ; Sequence 13, Application US/08022381A
 ; Patent No. 5478810
 ; GENERAL INFORMATION:
 ; APPLICANT: Stuber, Werner
 ; TITLE OF INVENTION: Peptide Amides, Processes for the
 ; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
 ; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 US-08-022-381A-13

APPLICANT: Fickenscher, Karl
 TITLE OF INVENTION: Peptide Amides, Processes for the
 TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
 TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESS: Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/022,381A
 FILING DATE: 24-FEB-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/696,085
 FILING DATE: 06-MAY-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 40 14 655.3
 FILING DATE: 08-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Markowicz, Karen R.
 REGISTRATION NUMBER: 36,351
 REFERENCE/DOCKET NUMBER: 05552.1054-01000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-022-381A-13

Query Match 100.0%; Score 25; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 29
 US-08-022-381A-14
 ; Sequence 14, Application US/08022381A
 ; Patent No. 5478810
 ; GENERAL INFORMATION:
 ; APPLICANT: Stuber, Werner
 ; TITLE OF INVENTION: Peptide Amides, Processes for the
 ; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
 ; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 US-08-022-381A-14

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,381A
; FILING DATE: 24-FEB-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 08-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 05552.1054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-022-381A-14

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 30
US-08-022-381A-15
; Sequence 15, Application US/08022381A
; Patent No. 5478810
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes for the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These as
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSER: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,381A
; FILING DATE: 24-FEB-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 08-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 05552.1054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 31
US-08-475-827A-2
; Sequence 2, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSER: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

US-08-475-827A-2

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 32

US-08-475-827A-3
; Sequence 3, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 06-MAY-1991
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-475-827A-3

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 33

US-08-475-827A-4
; Sequence 4, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-475-827A-4

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 34

US-08-475-827A-5
; Sequence 5, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22

Qy 1 GPRP 4
Db 1 GPRP 4

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-475-827A-5

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 35
US-08-475-827A-6
; Sequence 6, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-475-827A-6

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-475-827A-7

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 36
US-08-475-827A-7
; Sequence 7, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-475-827A-7

```

; FILING DATE: 06-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 14 655.3
; FILING DATE: 08-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-475-827A-7

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 37
US-08-475-827A-8
; Sequence 8, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION NUMBER:
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,381
; FILING DATE: 06-MAY-1991
; APPLICATION DATA:
; FILING DATE: 08-MAY-1990
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-475-827A-8

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 38
US-08-475-827A-9
; Sequence 9, Application US/08475827A
; Patent No. 5607858
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes For the
; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,827A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION NUMBER:
; FILING DATE: 24-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,085
; FILING DATE: 06-MAY-1991
; APPLICATION DATA:
; FILING DATE: 08-MAY-1990
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 05552.1054-02000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-475-827A-9

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 39

US-08-475-827A-10
 ; Sequence 10, Application US/08475827A
 ; Patent No. 5607858
 ; GENERAL INFORMATION:
 ; APPLICANT: Stuber, Werner
 ; APPLICANT: Fickenscher, Karl
 ; TITLE OF INVENTION: Peptide Amides, Processes For the
 ; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
 ; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475,827A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/022,381
 ; FILING DATE: 24-FEB-1993
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475,827A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/022,381
 ; FILING DATE: 24-FEB-1993
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/696,085
 ; FILING DATE: 06-MAY-1991
 ; APPLICATION NUMBER: DE 40 14 655.3
 ; FILING DATE: 08-MAY-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Johnson, Lori-Ann
 ; REGISTRATION NUMBER: 34,498
 ; REFERENCE/DOCKET NUMBER: 05552.1054-02000
 ; TELEPHONE: (202) 408-4400
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-475-827A-10

Query Match 100.0%; Score 25; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 40

US-08-475-827A-11
 ; Sequence 11, Application US/08475827A
 ; Patent No. 5607858

GENERAL INFORMATION:

APPLICANT: Stuber, Werner
 APPLICANT: Fickenscher, Karl
 TITLE OF INVENTION: Peptide Amides, Processes For the
 TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
 TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475,827A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/022,381
 FILING DATE: 24-FEB-1993
 APPLICATION NUMBER: US 07/696,085
 FILING DATE: 06-MAY-1991
 APPLICATION NUMBER: DE 40 14 655.3
 FILING DATE: 08-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Johnson, Lori-Ann
 REGISTRATION NUMBER: 34,498
 REFERENCE/DOCKET NUMBER: 05552.1054-02000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4400
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-475-827A-11

Query Match 100.0%; Score 25; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 41

US-08-475-827A-12
 ; Sequence 12, Application US/08475827A
 ; Patent No. 5607858
 ; GENERAL INFORMATION:
 ; APPLICANT: Stuber, Werner
 ; APPLICANT: Fickenscher, Karl
 ; TITLE OF INVENTION: Peptide Amides, Processes For the
 ; TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
 ; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Lori-Ann
REGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 05552.1054-02000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-827A-12

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 42
US-08-475-827A-13
Sequence 13, Application US/08475827A
Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
TITLE OF INVENTION: Peptide Amides, Processes For the Preparation Thereof And Agents Containing These As Fibrin/Thrombin Clotting Inhibitors
TITLE OF INVENTION: Peptide Amides, Processes For the Preparation Thereof And Agents Containing These As Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A

FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Lori-Ann
REGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 05552.1054-02000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-827A-13

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 43
US-08-475-827A-14
Sequence 14, Application US/08475827A
Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
TITLE OF INVENTION: Peptide Amides, Processes For the Preparation Thereof And Agents Containing These As Fibrin/Thrombin Clotting Inhibitors
TITLE OF INVENTION: Peptide Amides, Processes For the Preparation Thereof And Agents Containing These As Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-475-827A-15

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 45
US-08-595-718A-4
; Sequence 4, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb.Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Kuyas, C.
; AUTHORS: Haerberli, A.
; AUTHORS: Walder, P.
; AUTHORS: Straub, P. W.
; TITLE: Isolation of Human Fibrinogen and its
; TITLE: Derivatives by Affinity Chromatography on Gly-Pro-
; TITLE: Arg-Pro-Lys-Fractogel
; JOURNAL: Thromb. Haemost.
; VOLUME: 63
; ISSUE: 3
; PAGES: 439-444
; DATE: 28-JUN-1990

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US-08-595-718A-4

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 46
US-08-672-255-1
; Sequence 1, Application US/08572255
; Patent No. 5786458
; GENERAL INFORMATION:
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; APPLICANT: Lang, John M.
; APPLICANT: Galloway, Cynthia J.
; TITLE OF INVENTION: Selective Stabilization of Protein
; TITLE OF INVENTION: During Viral Inactivation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,255
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide

US-08-672-255-1

Query Match 100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 47
US-08-022-381A-16
; Sequence 16, Application US/08022381A
; Patent No. 5478810
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes for the
; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315

US-08-022-381A-16

Query Match 100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 48
US-08-022-381A-17
; Sequence 17, Application US/08022381A
; Patent No. 5478810
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Fickenscher, Karl
; TITLE OF INVENTION: Peptide Amides, Processes for the
; TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
; TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315

US-08-022-381A-16

Query Match 100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

US-08-022-381A-16

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Markowicz, Karen R.
/ REGISTRATION NUMBER: 36,351
/ REFERENCE/DOCKET NUMBER: 05552.1054-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-022-381A-18

Query Match 100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 GPPP 4
DB 1 ||||
1 GPPP 4

RESULT 50
US-08-022-381A-19
/ Sequence 19, Application US/08022381A
/ Patent No. 5478810
/ GENERAL INFORMATION:
/ APPLICANT: Stuber, Werner
/ APPLICANT: Fickenscher, Karl
/ TITLE OF INVENTION: Peptide Amides, Processes for the
/ TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
/ TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESSEE: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/022.381A
/ FILING DATE: 24-FEB-1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/696,085
/ FILING DATE: 06-MAY-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE 40 14 655.3
/ FILING DATE: 08-MAY-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Markowicz, Karen R.
/ REGISTRATION NUMBER: 36,351
/ REFERENCE/DOCKET NUMBER: 05552.1054-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-022-381A-19

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Query Match 100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
| | | |
Db 1 GPRP 4

Search completed: September 7, 2004, 19:01:24
Job time : 32 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:00:58 ; Search time 124 Seconds
(without alignments)
10.163 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Published Applications AA:*

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10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	4	9	US-09-779-054-16
2	25	100.0	4	10	US-09-931-009A-2
3	25	100.0	4	14	US-10-046-801-6
4	25	100.0	4	15	US-10-016-569A-25
5	25	100.0	4	15	US-10-308-644-25
6	25	100.0	5	9	US-09-953-657-4
7	25	100.0	5	12	US-10-619-520-1
8	25	100.0	5	12	US-10-619-520-2
9	25	100.0	6	12	US-10-414-523-23
10	25	100.0	6	12	US-10-414-524-28
11	25	100.0	7	15	US-10-449-659-14
12	25	100.0	9	9	US-09-730-379B-3
13	25	100.0	9	12	US-10-619-520-8
14	25	100.0	9	12	US-10-334-726-138
15	25	100.0	9	14	US-10-283-423-49

16	25	100.0	9	14	US-10-283-423-117
17	25	100.0	9	14	US-10-213-821-49
18	25	100.0	9	14	US-10-213-821-117
19	25	100.0	9	16	US-10-736-048-49
20	25	100.0	9	16	US-10-736-048-117
21	25	100.0	10	9	US-09-765-614B-10
22	25	100.0	10	9	US-09-925-715-7
23	25	100.0	10	10	US-09-572-404B-230
24	25	100.0	10	13	US-10-078-547-10
25	25	100.0	10	14	US-10-151-882-28
26	25	100.0	10	16	US-10-724-075-10
27	25	100.0	15	13	US-10-068-569-5
28	25	100.0	16	14	US-10-161-791-411
29	25	100.0	17	14	US-10-177-257-3
30	25	100.0	18	9	US-09-805-301-92
31	25	100.0	18	14	US-10-181-654-21
32	25	100.0	18	14	US-10-181-654-35
33	25	100.0	20	9	US-09-864-761-33658
34	25	100.0	20	14	US-10-225-567A-1348
35	25	100.0	20	16	US-10-416-249-102
36	25	100.0	21	9	US-09-729-835-94
37	25	100.0	21	11	US-09-833-245-551
38	25	100.0	21	16	US-10-373-809-94
39	25	100.0	22	8	US-08-424-550B-415
40	25	100.0	22	12	US-10-653-535-323
41	25	100.0	22	12	US-09-397-945-323
42	25	100.0	23	14	US-10-177-257-1
43	25	100.0	23	14	US-10-177-257-2
44	25	100.0	24	9	US-09-952-432A-5
45	25	100.0	26	9	US-09-726-643-104
46	25	100.0	26	9	US-09-864-761-36112
47	25	100.0	26	12	US-10-001-885-140
48	25	100.0	26	13	US-10-042-141-104
49	25	100.0	26	15	US-10-361-848-12
50	25	100.0	27	14	US-10-231-417-438
51	25	100.0	28	9	US-09-864-761-45472
52	25	100.0	30	15	US-10-361-811-293
53	25	100.0	30	15	US-10-369-186-293
54	25	100.0	32	9	US-09-864-761-47360
55	25	100.0	32	9	US-09-801-968-45
56	25	100.0	32	10	US-09-802-154-45
57	25	100.0	32	10	US-09-776-191-60
58	25	100.0	33	14	US-10-106-698-8047
59	25	100.0	34	14	US-10-029-386-28024
60	25	100.0	36	12	US-10-424-599-277739
61	25	100.0	37	12	US-10-424-599-285156
62	25	100.0	38	9	US-09-730-379B-9
63	25	100.0	38	9	US-09-730-379B-13
64	25	100.0	38	9	US-09-864-761-33686
65	25	100.0	38	14	US-10-029-386-31872

ALIGNMENTS

RESULT 1

US-09-779-054-16
; Sequence 15, Application US/09779054
; Patent No. US20020120102A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Xinjie
; APPLICANT: Kakkar, Vijay
; TITLE OF INVENTION: USE OF DENDROASPIN AS A SCAFFOLD FOR NON-DENDROASPIN DOMAINS
; FILE REFERENCE: A-70312/TAL/AMS
; CURRENT APPLICATION NUMBER: US/09/779,054
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: GB 0002625.2
; PRIOR FILING DATE: 2000-02-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT

Sequence 117, Appl
Sequence 49, Appl
Sequence 117, Appl
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Sequence 7, Appl
Sequence 230, Appl
Sequence 10, Appl
Sequence 28, Appl
Sequence 10, Appl
Sequence 5, Appl
Sequence 411, Appl
Sequence 3, Appl
Sequence 92, Appl
Sequence 21, Appl
Sequence 35, Appl
Sequence 33658, A
Sequence 1348, Ap
Sequence 102, App
Sequence 94, Appl
Sequence 551, App
Sequence 94, Appl
Sequence 415, App
Sequence 323, App
Sequence 1, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 104, App
Sequence 36112, A
Sequence 140, App
Sequence 104, App
Sequence 12, Appl
Sequence 438, App
Sequence 45472, A
Sequence 293, App
Sequence 293, App
Sequence 47360, A
Sequence 45, Appl
Sequence 60, Appl
Sequence 8047, Ap
Sequence 28024, A
Sequence 277739, A
Sequence 285156, A
Sequence 9, Appl
Sequence 13, Appl
Sequence 33686, A
Sequence 31872, A

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: thrombin-binding sequence
US-09-779-054-16

Query Match 100.0%; Score 25; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 2

US-09-931-009A-2
; Sequence 2, Application US/0991009A
; Publication No. US20030109431A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Theresa H.
; TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
; FILE REFERENCE: US 1257/01 (VA)
; CURRENT APPLICATION NUMBER: US/09/931,009A
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown. Obtained from a commercial source.
US-09-931-009A-2

Query Match 100.0%; Score 25; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 3

US-10-046-801-6
; Sequence 6, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1e1 Sequenc
US-10-046-801-6

Query Match 100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 4
US-10-016-569A-25
; Sequence 25, Application US/10016569A
; Publication No. US20030229013A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; TITLE OF INVENTION: the Same
; FILE REFERENCE: PI379
; CURRENT APPLICATION NUMBER: US/10/016,569A
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
US-10-016-569A-25

Query Match 100.0%; Score 25; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 5

US-10-308-644-25
; Sequence 25, Application US/10308644
; Publication No. US20030229017A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: PI379
; CURRENT APPLICATION NUMBER: US/10/308,644
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
US-10-308-644-25

Query Match 100.0%; Score 25; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 6

US-09-953-657-4
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; Dadd, Christopher A.
; Baumbach, George A.

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; OTHER INFORMATION: Synthesized peptide
US-10-619-520-2

Query Match          100.0%; Score 25; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRPP 4      |||||
Db       1 GRPP 4

RESULT 9
US-10-414-523-23
; Sequence 23, Application US/10414523
; Publication No. US20030211471A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD FOR DETECTING LIGANDS AND TARGETS IN A MIXTURE
; FILE REFERENCE: 221429
; CURRENT APPLICATION NUMBER: US/10/414,523
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/372,091
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-414-523-23

Query Match          100.0%; Score 25; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
Db 1 GPRP 4

RESULT 10

US-10-414-524-28
; Sequence 28, Application US/10414524
; Publication No. US20030212253A1
; GENERAL INFORMATION:
; APPLICANT: Hammond et al.
; TITLE OF INVENTION: PLASMA PROTEIN-BINDING LIGANDS
; FILE REFERENCE: 221948
; CURRENT APPLICATION NUMBER: US/10/414,524
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,091
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-414-524-28

Query Match 100.0%; Score 25; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
Db 1 GPRP 4

RESULT 11

US-10-449-659-14
; Sequence 14, Application US/10449659
; Publication No. US20030229005A1
; GENERAL INFORMATION:
; APPLICANT: Cognosci, Inc.
; APPLICANT: Moss, Marcia Lynn
; APPLICANT: Rasmussen, Fred H.
; APPLICANT: Vitek, Michael P.
; TITLE OF INVENTION: Assays for measuring matrix metalloproteinase activities
; FILE REFERENCE: 56816-5001-US
; CURRENT APPLICATION NUMBER: US/10/449,659
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/384,135
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: metalloproteinase substrate
US-10-449-659-14

Query Match 100.0%; Score 25; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
Db 1 GPRP 4

RESULT 12

QY 1 GPRP 4

US-09-730-379B-3
; Sequence 3, Application US/09730379B
; Patent No. US20010041670A1
; GENERAL INFORMATION:
; APPLICANT: Simantov M.D., Ronit
; APPLICANT: Silverstein M.D., Roy L.
; TITLE OF INVENTION: THROMBOSPONDIN-BINDING REGION OF HISTIDINE-RICH
; TITLE OF INVENTION: GLYCOPROTEIN AND METHODS OF USE
; FILE REFERENCE: 955-7F/CON
; CURRENT APPLICATION NUMBER: US/09/730,379B
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; JOURNAL: Biochemistry
; VOLUME: 25
; ISSUE: 8
; PAGES: 2220-2225
; DATE: 1986
; JOURNAL: Biochemistry
; VOLUME: 25
; ISSUE: 8
; PAGES: 2220-2225
; DATE: 1986
; DATABASE ACCESSION NUMBER: GenBank/P04196
US-09-730-379B-3

Query Match 100.0%; Score 25; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
Db 1 GPRP 4

RESULT 13

US-10-619-520-8
; Sequence 8, Application US/10619520
; Publication No. US20040057957A1
; GENERAL INFORMATION:
; APPLICANT: Robert, Koll
; APPLICANT: Richter, W.
; APPLICANT: Bieber, Franz
; APPLICANT: Tschoppe, W.
; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
; FILE REFERENCE: Attorney Docket No. US20040057957A1 1328/2
; CURRENT APPLICATION NUMBER: US/10/619,520
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(9)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Synthesized Peptide
US-10-619-520-8

Query Match 100.0%; Score 25; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

Db 1 GPRP 4
||||

RESULT 14

US-10-334-726-138
; Sequence 138, Application US/10334726
; Publication No. US20030211521A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
; TITLE OF INVENTION: BREAST CANCER ANTIGEN
; FILE REFERENCE: 1090-36
; CURRENT APPLICATION NUMBER: US/10/334,726
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/645,446
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00866
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: GB 9805877.9
; PRIOR FILING DATE: 1998-09-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: predicted
; OTHER INFORMATION: Peptide
US-10-334-726-138

Query Match 100.0%; Score 25; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
||||
DB 5 GPRP 8
||||

RESULT 15

US-10-283-423-49
; Sequence 49, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods
; FILE REFERENCE: PHEM002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-49

Query Match 100.0%; Score 25; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
||||
DB 3 GPRP 6
||||

RESULT 16

US-10-283-423-117
; Sequence 117, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods
; FILE REFERENCE: PHEM002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-117

Query Match 100.0%; Score 25; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
||||
DB 3 GPRP 6
||||

RESULT 17

US-10-213-821-49
; Sequence 49, Application US/10213821
; Publication No. US20030180297A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods
; FILE REFERENCE: 6297.2cp
; CURRENT APPLICATION NUMBER: US/10/213,821
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: No. US20030180297A1el Sequence
 US-10-213-821-49

Query Match 100.0%; Score 25; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 3 GPRP 6

RESULT 18

US-10-213-821-117
 Sequence 117, Application US/10213821
 Publication No. US20030180297A1

GENERAL INFORMATION:

APPLICANT: Pharmacia & Upjohn
 APPLICANT: Lowery, David E.
 APPLICANT: Smith, Valdin G.
 APPLICANT: Kubiak, Teresa M.
 APPLICANT: Larsen, Martha J.

TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
 TITLE OF INVENTION: Related To The Same

FILE REFERENCE: 6297.2cp

CURRENT APPLICATION NUMBER: US/10/213,821

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: 09/693,746

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/425,676

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 185

SOFTWARE: PatentIn version 3.1

SEQ ID NO 117

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: No. US20030180297A1el Sequence

US-10-213-821-117

Query Match 100.0%; Score 25; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 3 GPRP 6

RESULT 19

US-10-736-048-49
 Sequence 49, Application US/10736048
 Publication No. US20040121956A1

GENERAL INFORMATION:

APPLICANT: Lowery, David E.
 APPLICANT: Smith, Valdin G.
 APPLICANT: Kubiak, Teresa M.
 APPLICANT: Larsen, Martha J.

TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
 TITLE OF INVENTION: Related To The Same

FILE REFERENCE: 6297.1cp

CURRENT APPLICATION NUMBER: US/10/736,048

CURRENT FILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US/09/693,746

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/425,676

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 168

SOFTWARE: PatentIn version 3.1

SEQ ID NO 49

LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Novel Sequence
 US-10-736-048-49

Query Match 100.0%; Score 25; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 3 GPRP 6

RESULT 20

US-10-736-048-117

Sequence 117, Application US/10736048

Publication No. US20040121956A1

GENERAL INFORMATION:

APPLICANT: Lowery, David E.

APPLICANT: Smith, Valdin G.

APPLICANT: Kubiak, Teresa M.

APPLICANT: Larsen, Martha J.

TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods

TITLE OF INVENTION: Related To The Same

FILE REFERENCE: 6297.1cp

CURRENT APPLICATION NUMBER: US/10/736,048

CURRENT FILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US/09/693,746

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/425,676

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 168

SOFTWARE: PatentIn version 3.1

SEQ ID NO 117

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Novel Sequence

US-10-736-048-117

Query Match 100.0%; Score 25; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 3 GPRP 6

RESULT 21

US-09-765-614B-10

Sequence 10, Application US/09765614B

Patent No. US20020102215A1

GENERAL INFORMATION:

APPLICANT: Nycomed Imaging AS

TITLE OF INVENTION: Improvements in or relating to

TITLE OF INVENTION: diagnostic/therapeutic

TITLE OF INVENTION: agents

FILE REFERENCE: REF/Klaveness/054

CURRENT APPLICATION NUMBER: US/09/765,614B

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn ver. 2.1

SEQ ID NO 10

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial

; OTHER INFORMATION: Sequence:Biotinylated
; OTHER INFORMATION: fibrin-anti-polymerant peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Biotinylated-Gly
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: AMIDATION
US-09-765-614B-10

Query Match 100.0%; Score 25; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 22
US-09-925-715-7
; Sequence 7, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Biotinylated
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Biotin-Gly
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: AMIDATION
US-09-925-715-7

Query Match 100.0%; Score 25; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 23
US-09-572-404B-230
; Sequence 230, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 230
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

; OTHER INFORMATION: sequence located in MCP at 295-304 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-572-404B-230

Query Match 100.0%; Score 25; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 7 GPRP 10

RESULT 24
US-10-078-547-10
; Sequence 10, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP. A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: WIP sequence 410-419 a.a., human
US-10-078-547-10

Query Match 100.0%; Score 25; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 4 GPRP 7

RESULT 25
US-10-151-882-28
; Sequence 28, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-151-882-28

Query Match 100.0%; Score 25; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 4 GPRP 7

RESULT 26

US-10-722-075-10
; Sequence 10, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Biotinylated
; OTHER INFORMATION: fibrin-anti-polymerant peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Biotinylated-Gly
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: AMIDATION

Query Match 100.0%; Score 25; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 27

US-10-068-569-5
; Sequence 5, Application US/10088569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-068-569-5

Query Match 100.0%; Score 25; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 7 GPRP 10

RESULT 28

US-10-161-791-411
; Sequence 411, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 411:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-411

Query Match 100.0%; Score 25; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 3 GPRP 6

RESULT 29

US-10-177-257-3
; Sequence 3, Application US/10177257
; Publication No. US20030082768A1
; GENERAL INFORMATION:

APPLICANT: Baskerville, Donald Scott
APPLICANT: Bartel, David P.
TITLE OF INVENTION: Use of a Ribozyme to Join Nucleic Acids
TITLE OF INVENTION: and Peptides
FILE REFERENCE: 0399.1177-007
CURRENT APPLICATION NUMBER: US/10/177,257
PRIOR APPLICATION NUMBER: US/09/702,543
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: US 09/291,837
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/082,256
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 17
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: BIV-1 Tat peptide
US-10-177-257-3

Query Match 100.0%; Score 25; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 2 GPRP 5

RESULT 30
US-09-805-301-92
Sequence 92, Application US/09805301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-09-805-301-92

Query Match 100.0%; Score 25; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 3 GPRP 6

RESULT 31
US-10-181-654-21
Sequence 21, Application US/10181654
Publication No. US20030108957A1
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy and Biology
APPLICANT: Creighton University
APPLICANT: Otvos, Laszlo
APPLICANT: Blaszczyk-Thurin, Magdalena
APPLICANT: Rogers, Mark
APPLICANT: Lovas, Sandor
TITLE OF INVENTION: Biotidal Molecules, Macromolecular Targets and Methods of Product
TITLE OF INVENTION: Use
FILE REFERENCE: WST94BPCT
CURRENT APPLICATION NUMBER: US/10/181,654
CURRENT FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/177,565
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/237,599
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 18
TYPE: PRT
ORGANISM: Apis mellifera
US-10-181-654-21

Query Match 100.0%; Score 25; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 10 GPRP 13

RESULT 32
US-10-181-654-35
Sequence 35, Application US/10181654
Publication No. US20030108957A1
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy and Biology
APPLICANT: Creighton University
APPLICANT: Otvos, Laszlo
APPLICANT: Blaszczyk-Thurin, Magdalena
APPLICANT: Rogers, Mark
APPLICANT: Lovas, Sandor
TITLE OF INVENTION: Biotidal Molecules, Macromolecular Targets and Methods of Product
TITLE OF INVENTION: Use
FILE REFERENCE: WST94BPCT
CURRENT APPLICATION NUMBER: US/10/181,654
CURRENT FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/177,565

; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/237,599
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Apidaecin la
US-10-181-654-35

Query Match 100.0%; Score 25; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|||
Db 10 GPRP 13

RESULT 33
US-09-864-761-33658
; Sequence 33658, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33658

; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000266.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HELL100, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
; OTHER INFORMATION: EST_HUMAN HIT: W52599.1, EVALUE 1.10e-01
; OTHER INFORMATION: EST_HUMAN HIT: AW956935.1, EVALUE 7.60e-02
US-09-864-761-33658

Query Match 100.0%; Score 25; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|||
Db 9 GPRP 12

RESULT 34
US-10-225-567A-1348
; Sequence 1348, Application US/10225567A
; Publication No. US20030113799A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1348
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1348

Query Match 100.0%; Score 25; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|||
Db 15 GPRP 18

RESULT 35
US-10-416-249-102
; Sequence 102, Application US/10416249
; Publication No. US20040132121A1
; GENERAL INFORMATION:
; APPLICANT: Dalrymple, Brian P.
; APPLICANT: Kongsuwan, Kritaya
; APPLICANT: Wijffels, Gene L.
; APPLICANT: Jennings, Philip A.
; APPLICANT: Kemp, Gregory W.
; TITLE OF INVENTION: METHOD OF IDENTIFYING ANTIBACTERIAL
; FILE REFERENCE: CULLM42.001APC

<pre>; CURRENT APPLICATION NUMBER: US/10-416,249 ; CURRENT FILING DATE: 2003-11-10 ; PRIOR APPLICATION NUMBER: PCT/AU01/01436 ; PRIOR FILING DATE: 2001-11-08 ; PRIOR APPLICATION NUMBER: AU PR 1320 ; PRIOR FILING DATE: 2000-11-08 ; PRIOR APPLICATION NUMBER: AU PR 2919 ; PRIOR FILING DATE: 2001-02-06 ; NUMBER OF SEQ ID NOS: 678 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 102 ; LENGTH: 20 ; TYPE: PRT ; ORGANISM: Magnetospirillum magnetotacticum US-10-416-249-102</pre>	<pre>Query Match 100.0%; Score 25; DB 16; Length 20; Best Local Similarity 100.0%; Pred.No. 7.le+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	<pre>QY 1 GPRP 4 Db 16 GPRP 19</pre>	<pre>RESULT 36 US-09-729-835-94 ; Sequence 94, Application US/09729835 ; Patent No. US20010016647A1 ; GENERAL INFORMATION: ; APPLICANT: Ruben et al. ; TITLE OF INVENTION: 29 Human Secreted Proteins ; FILE REFERENCE: PZ015P1 ; CURRENT APPLICATION NUMBER: US/09/729,835 ; CURRENT FILING DATE: 2000-12-06 ; PRIOR APPLICATION NUMBER: 09/257,179 ; PRIOR FILING DATE: 1999-02-25 ; PRIOR APPLICATION NUMBER: 60/056,270 ; PRIOR FILING DATE: 1997-08-29 ; PRIOR APPLICATION NUMBER: 60/056,271 ; PRIOR FILING DATE: 1997-08-29 ; PRIOR APPLICATION NUMBER: 60/056,247 ; PRIOR FILING DATE: 1997-08-29 ; PRIOR APPLICATION NUMBER: 60/056,073 ; PRIOR FILING DATE: 1997-08-29 ; NUMBER OF SEQ ID NOS: 128 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 94 ; LENGTH: 21 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-729-835-94</pre>	<pre>Query Match 100.0%; Score 25; DB 9; Length 21; Best Local Similarity 100.0%; Pred.No. 7.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	<pre>QY 1 GPRP 4 Db 12 GPRP 15</pre>	<pre>RESULT 37 US-09-833-245-551 ; Sequence 551, Application US/09833245 ; Publication No. US200400103441 ; GENERAL INFORMATION: ; APPLICANT: Human Genome Sciences, Inc. ; TITLE OF INVENTION: Albumin Fusion Proteins ; FILE REFERENCE: PF546PCT ; CURRENT APPLICATION NUMBER: US/09/833,245 ; CURRENT FILING DATE: 2001-04-12 ; PRIOR APPLICATION NUMBER: 60/229, 358</pre>	<pre>PRIOR FILING DATE: 2000-04-12 PRIOR APPLICATION NUMBER: 60/256, 931 PRIOR FILING DATE: 2000-12-21 PRIOR APPLICATION NUMBER: 60/199, 384 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 2267 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 551 LENGTH: 21 TYPE: PRT ORGANISM: Homo sapiens US-09-833-245-551</pre>	<pre>Query Match 100.0%; Score 25; DB 11; Length 21; Best Local Similarity 100.0%; Pred.No. 7.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	<pre>QY 1 GPRP 4 Db 8 GPRP 11</pre>	<pre>RESULT 38 US-10-373-809-94 ; Sequence 94, Application US/10373809 ; Publication No. US20040023260A1 ; GENERAL INFORMATION: ; APPLICANT: Ruben et al. ; TITLE OF INVENTION: 29 Human Secreted Proteins ; FILE REFERENCE: PZ015P1 ; CURRENT APPLICATION NUMBER: US/10/373,809 ; CURRENT FILING DATE: 2003-02-27 ; PRIOR APPLICATION NUMBER: US/09/729,835 ; PRIOR FILING DATE: 2000-12-06 ; PRIOR APPLICATION NUMBER: 09/257,179 ; PRIOR FILING DATE: 1999-02-25 ; PRIOR APPLICATION NUMBER: 60/056,270 ; PRIOR FILING DATE: 1997-08-29 ; PRIOR APPLICATION NUMBER: 60/056,271 ; PRIOR FILING DATE: 1997-08-29 ; PRIOR APPLICATION NUMBER: 60/056,247 ; PRIOR FILING DATE: 1997-08-29 ; PRIOR APPLICATION NUMBER: 60/056,073 ; PRIOR FILING DATE: 1997-08-29 ; NUMBER OF SEQ ID NOS: 128 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 94 ; LENGTH: 21 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-373-809-94</pre>	<pre>Query Match 100.0%; Score 25; DB 16; Length 21; Best Local Similarity 100.0%; Pred.No. 7.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	<pre>QY 1 GPRP 4 Db 12 GPRP 15</pre>	<pre>RESULT 39 US-08-424-550B-415 ; Sequence 415, Application US/08424550B ; Publication No. US20020119447A1 ; GENERAL INFORMATION: ; APPLICANT: JOHN N. SIMONS ; APPLICANT: TAMI J. PILOT-MATIAS ; APPLICANT: GEORGE J. DAWSON ; APPLICANT: GEORGE C. SCHLAUDER ; APPLICANT: SURESH M. DESAI ; APPLICANT: THOMAS P. LEARY ; APPLICANT: ANTHONY SCOTT MUERHOFF</pre>
---	--	--	--	---	--	--	---	--	---	---	--	--	--

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Query Match	Best Local Similarity	100.0%;	Score 25;	DB 16;	Length 21;	
Matches	Matches	4;	Conservative	0;	Mismatches	0;
QY	QY	1 GPRP 4				
Db	Db	16 GPRP 19				
RESULT 36	RESULT 36					
US-09-729-835-94	US-09-729-835-94					
Sequence 94, Application US/09729835	Sequence 94, Application US/09729835					
Patent No. US20010016647A1	Patent No. US20010016647A1					
GENERAL INFORMATION:	GENERAL INFORMATION:					
APPLICANT: Ruben et al.	APPLICANT: Ruben et al.					
TITLE OF INVENTION: 29 Human Secreted Proteins	TITLE OF INVENTION: 29 Human Secreted Proteins					
FILE REFERENCE: PZ015P1	FILE REFERENCE: PZ015P1					
CURRENT APPLICATION NUMBER: US/09/729,835	CURRENT APPLICATION NUMBER: US/09/729,835					
PRIOR FILING DATE: 2000-12-06	PRIOR FILING DATE: 2000-12-06					
PRIOR APPLICATION NUMBER: 09/257,179	PRIOR APPLICATION NUMBER: 09/257,179					
PRIOR FILING DATE: 1999-02-25	PRIOR FILING DATE: 1999-02-25					
PRIOR APPLICATION NUMBER: 60/056,270	PRIOR APPLICATION NUMBER: 60/056,270					
PRIOR FILING DATE: 1997-08-29	PRIOR FILING DATE: 1997-08-29					
PRIOR APPLICATION NUMBER: 60/056,271	PRIOR APPLICATION NUMBER: 60/056,271					
PRIOR FILING DATE: 1997-08-29	PRIOR FILING DATE: 1997-08-29					
PRIOR APPLICATION NUMBER: 60/056,247	PRIOR APPLICATION NUMBER: 60/056,247					
PRIOR FILING DATE: 1997-08-29	PRIOR FILING DATE: 1997-08-29					
PRIOR APPLICATION NUMBER: 60/056,073	PRIOR APPLICATION NUMBER: 60/056,073					
PRIOR FILING DATE: 1997-08-29	PRIOR FILING DATE: 1997-08-29					
NUMBER OF SEQ ID NOS: 128	NUMBER OF SEQ ID NOS: 128					
SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 94	SEQ ID NO 94					
LENGTH: 21	LENGTH: 21					
TYPE: PRT	TYPE: PRT					
ORGANISM: Homo sapiens	ORGANISM: Homo sapiens					
US-09-729-835-94	US-09-729-835-94					
Query Match	Query Match	100.0%;	Score 25;	DB 9;	Length 21;	
Best Local Similarity	Best Local Similarity	100.0%;	Pred. No. 7.4e+02;			
Matches	Matches	4;	Conservative	0;	Mismatches	0;
QY	QY	1 GPRP 4				
Db	Db	12 GPRP 15				
RESULT 37	RESULT 37					
US-09-833-245-551	US-09-833-245-551					
Sequence 551, Application US/09833245	Sequence 551, Application US/09833245					
Patent No. US20040010134A1	Patent No. US20040010134A1					
GENERAL INFORMATION:	GENERAL INFORMATION:					
APPLICANT: Human Genome Sciences, Inc.	APPLICANT: Human Genome Sciences, Inc.					
TITLE OF INVENTION: Albumin Fusion Proteins	TITLE OF INVENTION: Albumin Fusion Proteins					
FILE REFERENCE: PF546PCT	FILE REFERENCE: PF546PCT					
CURRENT APPLICATION NUMBER: US/09/833,245	CURRENT APPLICATION NUMBER: US/09/833,245					
PRIOR FILING DATE: 2001-04-12	PRIOR FILING DATE: 2001-04-12					
PRIOR APPLICATION NUMBER: 60/229,358	PRIOR APPLICATION NUMBER: 60/229,358					

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Query Match	Best Local Similarity	100.0%;	Score 25;	DB 16;	Length 21;	
Matches 4;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 1 GPRP 4	Db 16 GPRP 19					
Db 16 GPRP 19						
RESULT 36						
US-09-729-835-94						
Sequence 94, Application US/09729835						
Patent No. US20010016647A1						
GENERAL INFORMATION:						
APPLICANT: Ruben et al.						
TITLE OF INVENTION: 29 Human Secreted Proteins						
FILE REFERENCE: PZ015P1						
CURRENT APPLICATION NUMBER: US/09/729,835						
PRIOR FILING DATE: 2000-12-06						
PRIOR FILING DATE: 1999-02-25						
PRIOR FILING DATE: 1997-08-29						
PRIOR FILING DATE: 1997-08-29						
PRIOR FILING DATE: 1997-08-29						
PRIOR FILING DATE: 1997-08-29						
PRIOR FILING DATE: 1997-08-29						
PRIOR FILING DATE: 1997-08-29						
PRIOR FILING DATE: 1997-08-29						
PRIOR FILING DATE: 1997-08-29						
NUMBER OF SEQ ID NOS: 128						
SOFTWARE: PatentIn Ver. 2.0						
SEQ ID NO 94						
LENGTH: 21						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-09-729-835-94						
Query Match	Best Local Similarity	100.0%;	Score 25;	DB 9;	Length 21;	
Matches 4;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 1 GPRP 4	Db 12 GPRP 15					
Db 12 GPRP 15						
RESULT 37						
US-09-833-245-551						
Sequence 551, Application US/09833245						
Publication No. US200400103441						
GENERAL INFORMATION:						
APPLICANT: Human Genome Sciences, Inc.						
TITLE OF INVENTION: Albumin Fusion Proteins						
FILE REFERENCE: PF546PCT						
CURRENT APPLICATION NUMBER: US/09/833,245						
PRIOR FILING DATE: 2001-04-12						
PRIOR APPLICATION NUMBER: 60/229, 358						

APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 415:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-415

Query Match 100.0%; Score 25; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 4 GPRP 7

RESULT 40
US-10-653-595-323
Sequence 323, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312

PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 323
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-323

Query Match 100.0%; Score 25; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 41
US-09-397-945-323
Sequence 323, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT APPLICATION NUMBER: US/09/397,945
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,581
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,577
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,313
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 323
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-09-397-945-323

Query Match 100.0%; Score 25; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4


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RESULT 42
US-10-177-257-1
; Sequence 1, Application US/10177257
; Publication No. US20030082768A1
; GENERAL INFORMATION:
; APPLICANT: Baskerville, Donald Scott
; APPLICANT: Bartel, David P.
; TITLE OF INVENTION: Use of a Ribozyme to Join Nucleic Acids
; TITLE OF INVENTION: and Peptides
; FILE REFERENCE: 0399.1177-007
; CURRENT APPLICATION NUMBER: US/10/177.257
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US/09/702.543
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 09/291.837
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/082,256
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Tat tag peptide 1
US-10-177-257-1
Query Match 100.0%; Score 25; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 5 GPRP 8

RESULT 43
US-10-177-257-2
; Sequence 2, Application US/10177257
; Publication No. US20030082768A1
; GENERAL INFORMATION:
; APPLICANT: Baskerville, Donald Scott
; APPLICANT: Bartel, David P.
; TITLE OF INVENTION: Use of a Ribozyme to Join Nucleic Acids
; TITLE OF INVENTION: and Peptides
; FILE REFERENCE: 0399.1177-007
; CURRENT APPLICATION NUMBER: US/10/177.257
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US/09/702.543
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 09/291.837
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/082,256
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Tat 2 tag peptide
US-10-177-257-2
Query Match 100.0%; Score 25; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 5 GPRP 8

RESULT 44
US-09-952-432A-5
; Sequence 5, Application US/09952432A
; Patent No. US20020150588A1
; GENERAL INFORMATION:
; APPLICANT: Allison, James P.
; APPLICANT: Passo, Marcella
; APPLICANT: Shastri, Nilabh
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
; FILE REFERENCE: 018941-0011005
; CURRENT APPLICATION NUMBER: US/09/952,432A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/234,472
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SPAS-1 cDNA
US-09-952-432A-5
Query Match 100.0%; Score 25; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 19 GPRP 22

RESULT 45
US-09-726-643-104
; Sequence 104, Application US/09726643
; Patent No. US2002028449A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/09/726,643
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,725
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-643-104
Query Match 100.0%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 6 GPRP 9

RESULT 46
US-09-864-761-36112
; Sequence 36112, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

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```

Query Match      100.0%; Score 25; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRRP 4
        ||||
Db      6 GRRP 9

RESULT 49
US-10-361-848-12
; Sequence 12, Application US/10361848
; Publication No. US20030221207A1

```

Qy	1	GPRP	4
Db	17	GPRP	20

Qy	1	GPRP	4
Db	17	GPRP	20

; GENERAL INFORMATION:
; APPLICANT: McMahon, Ellen
; APPLICANT: Qin, Wenning
; APPLICANT: Goellner, Joseph
; APPLICANT: Rudolph, Amy
; TITLE OF INVENTION: CARDIAC-SPECIFIC 11BETA-HYDROXYSTEROID
; TITLE OF INVENTION: DEHYDROGENASE TYPE 2 TRANSGENIC MICE
; FILE REFERENCE: 061765.000420
; CURRENT APPLICATION NUMBER: US/10/361,848
; CURRENT FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-361-848-12

Query Match 100.0%; Score 25; DB 15; Length 26;
Best Local Similarity 100.0%; Pred.No. 8.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 16 GPRP 19

RESULT 50
US-10-231-417-438
; Sequence 438, Application US/10231417
; Publication No. US2003017681A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: P2019P1
; CURRENT APPLICATION NUMBER: US/10/231,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 438
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-417-438

Query Match 100.0%; Score 25; DB 14; Length 27;
Best Local Similarity 100.0%; Pred.No. 9.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 18 GPRP 21

Search completed: September 7, 2004, 19:12:28
Job time : 126 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2004, 18:45:11 ; Search time 123 Seconds
(without alignments)
9.189 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	25	100.0	4	1	AAP61324	AAP61324 Sequence
2	25	100.0	4	2	AAR03320	AAR03320 Anti-coag
3	25	100.0	4	2	AAR32382	AAR32382 Fibrinogen
4	25	100.0	4	2	AAR49796	AAR49796 Sequence
5	25	100.0	4	2	AAR09861	AAR09861 Thrombin
6	25	100.0	4	2	AAR25198	AAR25198 GPRP-pept
7	25	100.0	4	2	AAR34568	AAR34568 Synthetic
8	25	100.0	4	2	AAR45491	AAR45491 Targeting
9	25	100.0	4	2	AAR52073	AAR52073 Sequence
10	25	100.0	4	2	AAR41677	AAR41677 Fibrin po
11	25	100.0	4	2	AAR31032	AAR31032 Non-cross
12	25	100.0	4	3	AAR32378	AAR32378 Cell diff
13	25	100.0	4	3	AAR54922	AAR54922 Fibrin po
14	25	100.0	4	3	AAR20589	AAR20589 Targeting
15	25	100.0	4	4	AAR98327	AAR98327 Acylated
16	25	100.0	4	5	AAR30381	AAR30381 Glycoprot
17	25	100.0	4	6	ABG74561	ABG74561 Oligopept
18	25	100.0	4	7	ABU63154	ABU63154 Targeting
19	25	100.0	4	7	ADD32227	ADD32227 Fibrin po
20	25	100.0	5	2	AAR15728	AAR15728 Anticoagu
21	25	100.0	5	2	AAR15720	AAR15720 Anticoagu
22	25	100.0	5	2	AAR15725	AAR15725 Anticoagu
23	25	100.0	5	2	AAR15722	AAR15722 Anticoagu
24	25	100.0	5	2	AAR15723	AAR15723 Anticoagu
25	25	100.0	5	2	AAR15721	AAR15721 Anticoagu

AAR15726 Anticoagu
AAR15724 Anticoagu
AAR15727 Anticoagu
AAR15719 Anticoagu
AAR15718 Anticoagu
AAR60333 Blood coa
AAR60330 Blood coa
AAR60334 Blood coa
AAR09863 Thrombin
AAR4570 Synthetic
AAR47188 Peptide 1
AAR2898 Fibrinogen
AAR92897 Fibrinogen
AAR18327 Fibrinogen
AAR18329 Fibrinogen
AAR15733 Anticoagu
AAR15730 Anticoagu
AAR15731 Anticoagu
AAR15732 Anticoagu
AAR15729 Anticoagu
AAR60332 Blood coa
AAR78985 Tc-99m la
AAR6867 Fibrinogen
AAR69317 Gp IIB/II
AAR69319 Gp IIB/II
AAR25199 GPRP-pept
AAR50606 Thrombin
AAR7903 Human JAG
AAR25504 Tc-99m la
AAR25469 Ligand #1
AAR54923 Peptide 1
AAR95519 Fibrin po
AAR08286 Matrix-me
AAR69317 Gp IIB/II
AAR50607 Thrombin
AAR2903 Fibrinogen
AAR55446 HLA bindi
AAR25505 Tc-99m la
AAR54924 Peptide 1
AAR95517 Fibrin po

ALIGNMENTS

RESULT 1	
AAP61324	
ID	AAP61324 standard; peptide; 4 AA.
XX	XX AAP61324;
AC	AC
DT	DT 24-OCT-2003 (revised)
DT	DT 27-AUG-2003 (revised)
DT	DT 03-OCT-2002 (revised)
DT	DT 23-JUL-1991 (first entry)
XX	XX Sequence of tetrapeptide of desAA-fibrin.
DE	DE
XX	XX Tissue plasminogen activator; fibrinolysis; assay; diagnosis.
KW	KW
XX	XX Coelognathus radiatus.
OS	OS Bothrops; genus".
XX	XX WO8605814-A.
PN	PN
XX	XX 09-OCT-1986.
PD	PD
XX	XX 27-MAR-1986; 86WO-SR000144.
PF	PF
XX	XX 01-APR-1985; 85SE-00001614.
PR	PR
XX	XX (BIOP-) BIOPOOL AB.
XX	XX (RANB/) RANBY M G.
PA	PA
PA	PA

XX
PI Ranby M;
XX WPI; 1986-278827/42.
XX Fibrin solubilised with tetra:peptide - used in diagnostic procedures for
PT determining fibrinolysis factors.
XX
PS Claim 2; Page 18; 22pp; English.
XX
CC The patentors claim a compsn. in which AAF61324 is pref. present at a
CC concn. of equal to or more than, 0.4 (pref. 2) mg./ml. of the compsn. The
CC compsn. can be used in diagnostic tests such as the determ. of the
CC enzyme tissue plasminogen activator as a standard in the detection of
CC trace amts. of fibrin in biological fluids. It may also be administered
CC in vivo to measure the total fibrinolytic capacity of an organism.
CC (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 27-AUG-2003
CC to correct OS field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPRP 4
Db |||||
1 GPRP 4
RESULT 2
ID AAR05320 standard; peptide; 4 AA.
AC AAR05320;
XX
XX 25-MAR-2003 (revised)
DT 08-OCT-1990 (first entry)
XX
XX Anti-coagulant peptide.
XX
XX Anti-coagulant; cerebral thrombosis; myocardial infarction.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 3 /label= ornithine.
FT Misc-difference 4 /label= proline or prolylproline.
XX
XX JPC2115197-A.
XX
XX 27-APR-1990.
XX
XX 21-OCT-1988; 88JP-00265809.
XX
XX 21-OCT-1988; 88JP-00265809.
XX
XX (DAUC) DAIICHI SEIYAKU CO.
XX
XX WPI; 1990-175285/23.
XX
XX Peptide contg. proline - is used for cerebral thrombosis, myocardial
PT infarction etc. due to anti-coagulation activity.
PT
PS Claim 1; Page 975; 10pp; Japanese.
XX
XX C-terminal is in amide form. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX Sequence 4 AA;
SQ

Query Match 100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPRP 4
Db |||||
1 GPRP 4
RESULT 3
ID AAR32382 standard; peptide; 4 AA.
XX
AC AAR32382;
XX
XX 25-MAR-2003 (revised)
DT 01-JUL-1993 (first entry)
XX
XX Fibrinogen binding peptide #6.
XX
XX platelet aggregation; fibrinogen A-alpha chain; protein scrambling;
KW GPR-like peptide.
XX
XX Synthetic.
XX
XX WO9304079-A1.
XX
XX 04-MAR-1993.
XX
XX 20-AUG-1992; 92WO-US006933.
XX
XX 21-AUG-1991; 91US-00813315.
XX
XX (RECE-) RECEPTOR LAB INC.
XX
XX Venton DL, Hopfinger AJ, Le Breton G;
PI WPI; 1993-093932/11.
XX
XX Identifying peptide(s) which bond to predetermined targets - by random
PT degradation and recombination of peptide(s) and isolating bound
PT peptide(s).
XX
XX Example 5; Page 58; 89pp; English.
XX
XX Synthetic peptides beginning with the sequence Gly-Pro-Arg (e.g. GPRP)
CC will bind to fibrinogen and prevent fibrin polymerisation. A scrambling
CC reaction was used to determine whether unique GPR-like peptides could be
CC created from a reaction seeded with GPR and if these new products could
CC bind to fibrinogen. See e.g. AAR32379. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPRP 4
Db |||||
1 GPRP 4
RESULT 4
ID AAR49796 standard; peptide; 4 AA.
XX
XX AAR49796;
XX
XX 25-MAR-2003 (revised)
DT 23-AUG-1994 (first entry)
XX
XX Sequence of peptide which binds to human fibrinogen.
DE

XX Random degradation; recombination; scrambling reaction.
 XX Synthetic.
 OS WO9404558-A1.
 PN 03-MAR-1994.
 PD 09-AUG-1993; 93WO-US008231.
 PF 21-AUG-1992; 92US-00932200.
 PR (RECE-) RECEPTOR LAB INC.
 XX Venton DL, Hopfinger AJ;
 XX WPI; 1994-083103/10.
 DR Identifying peptides which binds to a specific target - by contacting
 XX target with scrambled equilibrium mixt. of many peptide derived from
 PT protein by incubation with protease, for detecting potential therapeutic
 PT agents.
 XX Example; Page 54; 97pp; English.
 PS The inventors claim a method for inexpensively and rapidly producing a
 XX large and varied population of peptides and screening this varied
 CC population for the presence of peptides which bind to a target, for
 CC example, a macromolecule associated with a particular physiological
 CC function. The specific binding peptides are isolated and sequenced,
 CC synthesised on a large-scale, their biological activity is demonstrated,
 CC and then subjected to clinical testing. The random population of peptides
 CC is generated by employing a scrambling system which utilises one or more
 CC proteases, esp. pepsin, bromelain, thermolysin, trypsin, pronase,
 CC chymotrypsin, subtilisin and dipeptidyl peptidase IV. A typical starting
 CC protein is casein. Targets are esp. receptors involved in physiological
 CC processes, partic. fibrinogen; sickle cell haemoglobin; collagenase IV;
 CC rennin; Gp. IIB IIIa or phospholipase A2. It has been demonstrated that
 CC synthetic peptides beginning with the sequence GPR will bind to
 CC fibrinogen. Such peptides include GPR, GPRP and GPRV. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 5
 AAW09861
 ID AAW09861 standard; peptide; 4 AA.
 XX AAW09861;
 AC 30-JUN-1997 (first entry)
 XX Thrombin inhibitor.
 XX Thrombin; inhibitor; aggregation; platelet; determination; assay;
 KW qualitative; quantitative; fibrin.
 XX Synthetic.
 OS EP661383-A2.
 PN 05-JUL-1995.
 PD
 XX
 15-DEC-1994; 94EP-00119803.
 XX 30-DEC-1993; 93DE-04344919.
 PR (SEHW) BEHRINGWERKE AG.
 PA Reers M;
 XX WPI; 1995-233339/31.
 DR Determn. of thrombin-induced platelet aggregation in presence of fibrin -
 XX comprises use of fibrin aggregation inhibitor to suppress fibrin clot
 PT formation.
 PT Claim 4; Col 5; 5pp; German.
 XX In the qualitative or quantitative determ. of thrombin-induced platelet
 CC aggregation in the presence of fibrin, interference from fibrin clot
 CC formation is suppressed with a fibrin-aggregation inhibitor (e.g.
 CC AAW09861-63). The assay may be used to determine the platelet aggregation
 CC inhibitory activity of thrombin inhibitors. The peptides inhibit fibrin
 CC clot formation at high thrombin concns. without inhibiting platelet
 CC aggregation
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 6
 AAW25198
 ID AAW25198 standard; peptide; 4 AA.
 XX AAW25198;
 AC 05-JAN-1998 (first entry)
 XX GPRP-peptide capable of binding cell adhesion molecules.
 XX GPRP; glycine; proline; arginine; proline; bladder irrigation;
 KW cell adhesion molecule; binding; tumour removal; endoscopic operation;
 KW transurethral resection; cancer; neoplasia.
 XX Synthetic.
 OS DE19529909-A1.
 PN 20-FEB-1997.
 PD 15-AUG-1995; 95DE-01029909.
 PF 15-AUG-1995; 95DE-01029909.
 PR (PREP) PRESENIUS AG.
 XX Boehle A;
 XX WPI; 1997-133793/13.
 DR Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
 XX adhesion molecules.
 XX Claim 9; Page 8; 8pp; German.
 XX AAW25198 and AAW25199 are peptides containing a GPRP sequence. The
 CC peptides are capable of binding to cell adhesion molecules and are used
 CC in aqueous irrigation solutions for use during and after endoscopic

CC operations. Preferred irrigation solutions are electrolyte-free and
 CC contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing
 CC the amino acid sequences: RGP, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV
 CC and/or REDV (given in one letter amino acid code). The solutions are
 CC especially used for irrigating the bladder during and after tumour
 CC removal by transurethral resection. The peptides protect against
 CC recurrence of tumours
 XX
 SQ

Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 7

AAW34568
 ID AAW34568 standard; peptide; 4 AA.

XX
 AC AAW34568;

XX 05-MAR-1998 (first entry)

XX Synthetic fibrinogen binding peptide 1.

XX Fibrinogen binding peptide; fibrinopeptide A; fibrinogen isolation.

XX Synthetic.

XX WO9726280-A1.

XX 24-JUL-1997.

XX 14-JAN-1997; 97WO-AU000013.

XX 16-JAN-1996; 96AU-00007564.

XX (CSLC-) CSL LTD.

XX Xanellos J, Pham H, Oates A, Goss N;

XX WPI; 1997-385298/35.

XX Recovery of fibrinogen using polysaccharide solid support coupled to
 fibrinogen-binding peptide - requires only mild elution buffers.

XX Claim 5; Page 14; 24pp; English.

XX Peptides AAW34568-71 are synthetic fibrinogen binding peptides. A
 CC tripeptide, Gly-Pro-Arg is also claimed. This tripeptide sequence
 CC corresponds to the first 3 amino acids of the alpha-chain exposed by the
 CC thrombin catalysed release of the fibrinopeptide A in all vertebrate
 CC species. In the present peptide, the addition of a proline residue at
 CC position 4 increases the affinity of the peptide for fibrinogen almost
 CC tenfold. These synthetic fibrinogen binding peptides are immobilised on a
 CC novel polysaccharide support (e.g. Sephadex), to which they are coupled
 CC through a spacer or linker moiety. This linker moiety comprises a chain
 CC of greater than 7 atoms. The solid support is useful for the recovery and
 CC isolation of fibrinogen from material such as plasma, plasma fractions
 CC and fibrinogen-containing cell culture media arising from the production
 CC of fibrinogen by recombinant DNA techniques. The process is superior to
 CC other known affinity isolation procedures in that only mild elution
 CC buffers are required to recover the bound fibrinogen
 XX

Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 8

AAW45491
 ID AAW45491 standard; peptide; 4 AA.

XX
 AC AAW45491;

XX 20-MAY-1998 (first entry)

XX Targeting ligand directed to the glycoprotein GPIIb/IIIa receptor.

XX Contrast agent; targeted composition; diagnosis; diseased tissue;

KW glycoprotein GPIIb/IIIa receptor.

XX Synthetic.

XX Homo sapiens.

XX WO9640285-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009938.

XX 07-JUN-1995; 95US-00497684.

XX 01-MAY-1996; 96US-00640464.

XX (IMAR-) IMARX PHARM CORP.

XX Unger EC, Shen D, Wu G;

XX WPI; 1997-077233/07.

XX Contrast agent or targeted compen. for imaging or treating diseased
 tissue - comprising lipid, protein or polymer, a gas, and a targeting
 ligand e.g. a protein, peptide, saccharide or steroid.

XX Disclosure; Page 55; 175pp; English.

XX This sequence represents a targeting ligand directed to the GPIIb/IIIa
 CC receptor. The invention relates to a contrast agent for diagnostic
 CC imaging or a target composition which comprises: (i) a lipid, protein or
 CC polymer and (ii) a gas, in combination with (iii) a targeting ligand
 CC (Ti). Ti targets cells or receptors selected from myocardial,
 CC endothelial, epithelial and tumour cells and the glycoprotein GPIIb/IIIa
 CC receptor. Also claimed are: a composition comprising vesicles containing
 CC (i) - (iii) and an aqueous carrier; a targeted vesicle composition
 CC comprising a fluorinated gas and a targeting ligand (Ti) which targets
 CC tissues or receptors; a formulation for therapeutic or diagnostic use
 CC comprising (i)-(iii) and a bioactive agent; and a method for providing an
 CC image of an internal region of a patient, or for diagnosing the presence
 CC of diseased tissue, comprising: (a) administration of a composition as
 CC above; and (b) scanning the patient using ultrasound to obtain a viable
 CC image of the region or diseased tissue. The methods and compounds are
 CC useful for imaging or diagnosing the presence of diseased tissue,
 CC especially myocardial, endothelial or epithelial tissue but also
 CC gastrointestinal and cardiovascular regions. In particular the ligand
 CC targets regions of arteriosclerosis. Stabilised vesicles are particularly
 CC useful for perfusion imaging. The vesicles may also be used to deliver
 CC active agents to an intended target such as tissue or a receptor, and
 CC ultrasound can then be used to promote rupture of the vesicles and
 CC release a bioactive or diagnostic agent
 XX

Sequence 4 AA;

Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 1 GPRP 4
 ||||
 1 GPRP 4

RESULT 9
 AAW52073 ID AAW52073 standard; peptide; 4 AA.
 XX AC AAW52073;
 XX DT 25-MAR-2003 (revised)
 XX DT 23-SEP-1998 (first entry)
 XX DE Sequence contained in fibrin-specific targeting compound.
 XX XX Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
 XX KW thrombus.
 XX OS Synthetic.
 XX FN WO9824917-A1.
 XX PD 11-JUN-1998.
 XX XX 02-DEC-1997; 97WO-US021918.
 XX PF 02-DEC-1996; 96US-00753781.
 XX PR (DIAT-) DIATIDE INC.
 XX PA (UYSC-), UNIV SOUTHERN CALIFORNIA.
 XX PI Markland FS, Bush LR, Swenson S, Flores Sanchez E;
 XX DR WPI; 1998-333336/29.
 XX PT New thrombolytic agents - comprise thrombolytic proteinase covalently
 PT linked to targeting compound for binding to component of thrombus.
 XX PS Claim 9; Page 63; 79pp; English.
 XX CC The invention relates to new thrombolytic agents which comprise a
 CC thrombolytic proteinase covalently linked to a targeting compound capable
 CC of specifically binding to a component of a thrombus. The thrombolytic
 CC agents can be used for eliminating thrombi in vivo in, e.g. myocardial
 CC infarction, cerebral ischaemia, deep vein thrombosis or pulmonary
 CC embolism. A labelled form of the thrombolytic agent can also be used to
 CC image thrombi for diagnostic purposes. The thrombolytic agents are
 CC specifically targeted to thrombus sites in vivo and have minimal
 CC haemorrhagic side effects and side effects related to non-specific
 CC proteolysis. Multiple copies of the present amino acid sequence (GPRP)
 CC may be used in a fibrin-specific targeting compound. (Updated on 25-MAR-
 CC 2003 to correct PI field.)
 XX SQ Sequence 4 AA;
 Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 1 GPRP 4
 ||||
 1 GPRP 4

RESULT 10
 AAY41677 ID AAY41677 standard; peptide; 4 AA.
 XX AC AAY41677;
 XX DT 07-DEC-1999 (first entry)
 XX DT 07-DEC-1999 (first entry)
 XX XX

DE Fibrin polymerisation inhibitor peptide.
 XX Fibrin polymerisation inhibitor; factor Xa; thrombin; factor VIII;
 KW factor IX; factor X; coagulation factor; blood; photometric;
 KW Protein C anticoagulant pathway; thromboembolic disease;
 KW deep venous thrombosis; pulmonary embolism.
 XX OS Synthetic.
 XX XX WO9947699-A1.
 XX PD 23-SEP-1999.
 XX PF 11-MAR-1999; 99WO-EP001599.
 XX PR 19-MAR-1998; 98EP-00105043.
 XX XX (CHRO-) CHROMOGENIX AB.
 XX PI Rosen BS, Hall CMY;
 XX DR WPI; 1999-571846/48.
 XX PT New assays for determination of activity of components in the Protein C
 PT anticoagulant pathway, used for the study of diseases such as deep venous
 PT thrombosis and pulmonary embolism.
 XX PS Claim 27; Page 50; 67pp; English.
 XX CC Assays have been developed for the determination of activity of
 CC components in the Protein C anticoagulant pathway using additional metal
 CC ions to improve the sensitivity of the assays. An in vitro photometric
 CC method for qualitative screening and quantitative determination of the
 CC functional activity of components of the Protein C anticoagulant pathway
 CC of blood coagulation, comprises measuring the conversion rate of an
 CC exogenous substrate by an enzyme. The activity of the enzyme is related
 CC to the Protein C anticoagulant activity, in a blood sample of a human
 CC comprising coagulation factors and the exogenous substrate after at least
 CC partial activation of coagulation through the intrinsic, extrinsic, or
 CC common pathway and triggering coagulation by: (1) adding calcium ions;
 CC and (2) comparing the conversion rate with the conversion rate of a
 CC normal human blood sample determined in the same way, characterized by
 CC adding further metal(s) ions selected from divalent metal ions and
 CC monovalent copper ions to the sample. The method can be used for the
 CC global screening for defects in the Protein C anticoagulant pathway of
 CC blood coagulation, for determination of free Protein S activity in a
 CC blood sample, for determination of Protein C activity in a blood sample,
 CC and for screening for Factor V mutations in a blood sample. It allows
 CC improved screening and diagnosing of defects in the Protein C
 CC anticoagulant pathway in investigation of patients with thromboembolic
 CC diseases such as deep venous thrombosis and/or pulmonary embolism. The
 CC present sequence represents a fibrin polymerisation inhibitor for use in
 CC a method described in the present invention
 XX SQ Sequence 4 AA;
 Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 1 GPRP 4
 ||||
 1 GPRP 4

RESULT 11
 AAY31032 ID AAY31032 standard; peptide; 4 AA.
 XX AC AAY31032;
 XX DT 21-OCT-1999 (first entry)
 XX XX

DE Non-crosslinked protein particle peptide 81.
 XX
 KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KW albumin; haemoglobin; nanometer; micrometer; clearance.
 XX
 OS Synthetic.
 XX
 PN US5945033-A.
 XX
 PD 31-AUG-1999.
 XX
 XX 12-NOV-1996; 96US-00747137.
 XX
 PR 15-JAN-1991; 91US-00641720.
 PR 13-OCT-1992; 92US-00959560.
 PR 01-JUN-1993; 93US-00069831.
 PR 14-MAR-1994; 94US-00212546.
 XX
 PA (HEMO-) HEMOSPHERE INC.
 XX
 PI Yen RCK;
 XX
 DR WPI; 1999-508153/42.
 XX
 PT Non-crosslinked protein particles for therapeutic and diagnostic use.
 XX
 PS Example 22; Col 83-84; 65pp; English.
 XX
 CC This invention describes a novel aqueous suspension of monodisperse
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
 CC stable against dissolving upon dilution with an alcohol-free aqueous
 CC medium. The method involves (a) forming an aqueous solution containing
 CC albumin and hemoglobin and (b) treating the aqueous solution with an
 CC alcohol to cause the solution to become turbid. The particles are useful
 CC as agents for in vivo administration, either of their own administration
 CC or as a vehicle for other therapeutic or diagnostic agents. The method
 CC permits the formation of albumin and hemoglobin particles in the
 CC nanometer and micrometer size range, in a form closer to their natural
 CC form than the forms of the prior art. The particles therefore constitute
 CC a more closely controlled agent for in vivo administration, with greater
 CC ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 25; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db ||||
 1 GPRP 4
 RESULT 12
 AAY32378
 ID AAY32378 standard; peptide; 4 AA.
 XX
 AC AAY32378;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Cell differentiation, proliferation and maintenance factor peptide.
 XX
 KW Cell differentiation; cell proliferation; cell maintenance;
 KW ectoderm-like cell; embryonic stem cell; pluripotent cell; gene therapy;
 KW cell therapy; tissue transplant; organ transplant; xenotransplant;
 KW allotransplant; concomitant transplantation; transgenic animal.
 XX
 OS Synthetic.
 XX
 PN W09953021-A1.
 XX

PD 21-OCT-1999.
 XX
 PF 09-APR-1999; 99WO-AU000265.
 XX
 PR 09-APR-1998; 98AU-00002912.
 PR 23-SEP-1998; 98AU-00006097.
 XX
 PA (BRES-) BRESAGEN LTD.
 XX
 PI Bettess MD, Rathjen PD, Rathjen J;
 XX
 DR WPI; 2000-061970/05.
 XX
 PT New isolated biologically active factor capable of influencing
 PT differentiation, proliferation or maintenance of pluripotent cells.
 XX
 PS Claim 3; Page 122; 189pp; English.
 XX
 CC This sequence represents a peptide that can form the low mol.wt.
 CC component of a novel biologically active factor that is capable of
 CC influencing the differentiation, proliferation and/or maintenance of
 CC pluripotent cells. The factor consists of a low mol.wt. component
 CC selected from Pro, Pro-Ala, Ala-Pro-Gly, Pro-OH-Pro, Pro-Gly, Gly-Pro-
 CC Ala, Gly-Pro-OH-Pro, a peptide given in AAY32378-82, or a protease
 CC digested (including collagenase digested) collagen fragment, and a high
 CC mol.wt. component such as fibronectin. The biologically active factor is
 CC obtained from conditioned media of hepatic or hepatoma cells or cell
 CC lines or extraembryonic endodermal cells or cell lines. The factor is
 CC capable of causing the transition of pluripotent cells (e.g. embryonic
 CC stem cells in adherent culture and in suspension culture) to pluripotent
 CC cells having different properties, more specifically primitive ectoderm-
 CC like (EPL) cells. The factor is also capable of maintaining and
 CC supporting proliferation of these cells in vitro. It also allows the
 CC isolation and maintenance of EPL cells derived from in vitro and in vivo
 CC primitive ectoderm. These cells can be used in allo-, concomitant- or
 CC xeno-transplantation, cell therapy, tissue and organ augmentation or
 CC replacement, and gene therapy. They can also be used for producing
 CC chimeric or transgenic animals
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 25; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db ||||
 1 GPRP 4
 RESULT 13
 AAY54922
 ID AAY54922 standard; peptide; 4 AA.
 XX
 AC AAY54922;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Fibrin polymerisation site.
 XX
 KW Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m;
 KW GPIIb/IIIa receptor; cyclic peptide ligand.
 XX
 OS Synthetic.
 XX
 PN US5968476-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 07-JUN-1995; 95US-00484773.
 XX
 PR 21-MAY-1992; 92US-00886052.
 PR 11-JUL-1994; 94US-00273274.

XX (DIAT-) DIATIDE INC.
 XX Dean RT, Lister-James J;
 XX WPI; 2000-021733/02.
 XX A complex used for thrombus imaging comprises technetium-99m complexed
 PT with a peptide ligand for GPIIb/IIIa receptor.
 XX Claim 7; Col 31-32; 18pp; English.
 XX This sequence represents the fibrin polymerisation site. The invention
 CC relates to a complex (A) for thrombus imaging comprises technetium-99m
 CC (Tc-99m) complexed with a reagent comprising a peptide (P) with 4 to 100
 CC amino acids sequence and a Tc-99m binding moiety covalently bound to (P).
 CC (P) is selected from a linear peptide ligand for a GPIIb/IIIa receptor
 CC not comprising the amino acid sequence (arginine-glycine-aspartate), a
 CC peptide ligand for a polymerisation site of fibrin, and a cyclic peptide
 CC ligand for the GPIIb/IIIa receptor. The thrombus imaging reagents
 CC provided by the present invention can be used for visualising thrombi in
 CC a mammalian body when Tc-99m is labelled
 XX
 XX Sequence 4 AA;
 SQ Query Match 100.0%; Score 25; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB |||||
 1 GPRP 4

RESULT 14
 AAB20589
 ID AAB20589 standard; peptide; 4 AA.
 XX AAB20589;
 AC
 XX 12-DEC-2000 (first entry)
 DT
 XX Targeting ligand peptide #5.
 DE
 XX Targeting ligand peptide; imaging; ultrasound; vesicle; tumour;
 KW myocardial; endothelial; epithelial; glycoprotein GPIIb/IIIa receptor;
 KW detection; thrombus; integrin; malignancy; inflammation; lesion;
 KW atherosclerotic plaque; carcinoma.
 XX
 XX Synthetic.
 OS
 XX WO200045856-A2.
 FN
 XX 10-AUG-2000.
 PD
 XX 02-FEB-2000; 2000WO-US002620.
 PF
 XX 03-FEB-1999; 99US-00243640.
 PR
 XX (INAR-) INARX PHARM CORP.
 PA
 XX Ungr EC, Wu Y;
 PI
 XX WPI; 2000-532867/48.
 DR
 XX Ultrasound method, useful for diagnosis of e.g. thrombi or carcinomas,
 PT uses different types of energy for priming and interrogating the subject.
 PT
 XX Disclosure; Page 68; 21pp; English.
 PS
 XX The present invention describes an ultrasound method comprising: (i)
 CC administering a targeted vesicle composition (A); and (ii) scanning the
 CC subject by exposure to a first type of ultrasound energy and then

CC interrogating with a second type of ultrasound energy. (A) consists of a
 CC vesicle comprising a lipid, protein or polymer, encapsulating a gas, in
 CC combination with a targeting ligand. The method is used to detect: (i) a
 CC thrombus (particularly old or echogenic); (ii) a low concentration of
 CC vesicles; or (iii) vesicles targeted to endothelial tissue, particularly
 CC those containing integrins associated with malignancy or inflammation in
 CC early or small lesions, e.g. atherosclerotic plaque or ovarian,
 CC endometrial or other carcinomas. The method increases the signal from
 CC microbubbles and reduces background noise. The present sequence
 CC represents a targeting ligand peptide which is used in the method of the
 XX present invention
 XX Sequence 4 AA;
 SQ Query Match 100.0%; Score 25; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB |||||
 1 GPRP 4

RESULT 15
 AAB98927
 ID AAB98927 standard; peptide; 4 AA.
 XX AAB98927;
 AC
 XX 14-AUG-2001 (first entry)
 DT
 XX Acylated amino protecting method fibrinogen peptide.
 DE
 XX Acylated amino protection; chemical synthesis; drug delivery;
 KW bioavailability; biostability.
 KW
 XX Synthetic.
 OS
 XX WO200125170-A1.
 FN
 XX 12-APR-2001.
 PD
 XX 16-AUG-2000; 2000WO-US040671.
 PF
 XX 04-OCT-1999; 99US-0157435P.
 PR
 XX 30-JUN-2000; 2000US-00609565.
 PR
 XX (UYCA-) UNIV CALIFORNIA SAN DIEGO.
 PA
 XX Goodman M, Creighton CJ;
 PI
 XX WPI; 2001-389649/41.
 DR
 XX New protected amino-substituted compounds bearing acylated N-methyl-alpha
 PT -aminoisobutyryl moiety as amino protecting group, useful e.g. in organic
 PT synthesis and in the formulation/delivery of prodrugs with improved
 PT bioavailability.
 PT
 XX Disclosure; Page 12; 39pp; English.
 PS
 XX The present invention describes protected amino-substituted compounds
 CC with an acylated N-methyl-alpha-aminoisobutyryl (NMeAib) moiety as the
 CC amino protecting group. These can be used in chemical synthesis and in
 CC drug delivery. They can be used as prodrugs which have improved
 CC biostability or bioavailability. The present sequence is a peptide
 CC described in the exemplification of the invention
 XX
 XX Sequence 4 AA;
 SQ Query Match 100.0%; Score 25; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB ||||
1 GPRP 4

RESULT 16
ABG30381
ID ABG30381 standard; peptide; 4 AA.
XX AC
XX AC ABG30381;
XX DT 07-OCT-2002 (first entry)
XX DE Glycoprotein GPIIb/IIIa receptor targeting ligand #3.
XX KW Target vesicle; diagnostic imaging; thrombus; cancer; arteriosclerosis;
KW atherosclerotic plaque; infarcted myocardium;
KW glycoprotein GPIIb/IIIa receptor.
XX KW
XX OS Synthetic.
XX PN W0200236161-A2.
XX XX
XX PD 10-MAY-2002.
XX PF 17-OCT-2001; 2001WO-US032308.
XX PR 30-OCT-2000; 2000US-00699679.
XX PA (IMAR-) IMARX THERAPEUTICS INC.
XX PI Unger EC, Matsunaga TO, Schumann PA;
XX WPI; 2002-489986/52.
XX PT New targeted compound useful in target vesicle composition for imaging a
PT thrombus in a region of a patient has a combination of hydrophobic
PT compound, hydrophilic polymer and targeting ligand.
XX PS Disclosure; Page 65; 206pp; English.
XX CC This invention relates to a novel targeted compound having a combination
CC of hydrophobic compound, hydrophilic polymer and targeting ligand. The
CC invention also comprises a target vesicle composition comprising lipid,
CC protein or polymer gas filled vesicles in an aqueous carrier, a method
CC for imaging a thrombus in a region of a patient involving administering
CC to the patient a target vehicle composition and scanning the region
CC (preferably cardiac region) with diagnostic imaging (preferably
CC diagnostic ultrasound) and a method for lysing a thrombus in a blood
CC vessel. The invention also comprises a method for providing an image of
CC an internal region of a patient which can be used to obtain a visible
CC image of a region (preferably arteriosclerosis, atherosclerotic plaque,
CC infarcted myocardium or a cancer cell) and a method for diagnosing the
CC presence of disease tissue in a patient involving administering a target
CC vehicle composition and scanning the patient using ultrasound to obtain a
CC visible image of the region. The methods of the invention may be used for
CC imaging a thrombus in a region of a patient, lysing a thrombus in a blood
CC vessel, diagnosing the presence of diseased tissue in a patient and for
CC the therapeutic delivery in vivo of a bioactive agent. The compounds of
CC the invention are easily synthesised and have diagnostic efficacy,
CC enhanced biocompatibility and/or improved targeting efficacy over prior
CC art methods. The present sequence represents a targeting ligand to the
CC glycoprotein GPIIb/IIIa receptor used in the method of the invention
XX SQ Sequence 4 AA;

Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB ||||
1 GPRP 4

RESULT 17
ABG74561
ID ABG74561 standard; peptide; 4 AA.
XX AC
XX AC ABG74561;
XX DT 24-APR-2003 (first entry)
XX DE Oligopeptide fragment #2.
XX KW Cytostatic; antibacterial; tumour cell adhesion inhibitor; vaccine;
KW bladder carcinoma; transurethral resection; antimicrobial;
KW human medicine; veterinary medicine.
XX OS Unidentified.
XX PN DE10123348-A1.
XX PD 21-NOV-2002.
XX PF 14-MAY-2001; 2001DE-01023348.
XX PR 14-MAY-2001; 2001DE-01023348.
XX PA (PREP) PRESENIUS KABI DEUT GMBH.
XX PI Dormann D, Eichner W, Sommermeyer K, Volker L;
XX WPI; 2003-168758/17.
XX PT New DNA construct encoding polypeptide that includes cleavage sites,
PT useful for preparation of pharmaceutical peptides or their mixtures.
XX PS Disclosure; Page 3; 12pp; German.
XX CC This invention describes a novel DNA construct encoding a polypeptide
CC comprising several oligopeptide units and including recognition sites for
CC peptide cleavage. The products of the invention have cytostatic and
CC antibacterial activity, inhibit tumour cell adhesion and can be used to
CC prepare vaccines. The constructs are used for recombinant production of
CC peptides or their mixtures for use as pharmaceuticals, e.g. a mixture of
CC peptides used, in a rinse solution, to reduce the high rate of relapse in
CC superficial bladder carcinoma after transurethral resection or as
CC antimicrobial peptides for control of antibiotic-resistant bacteria in
CC human or veterinary medicine. The constructs allow the possible
CC production of peptides, or specific mixtures of them, at high
CC concentration and reduced cost. This sequence represents an oligopeptide
CC described in the disclosure of the invention
XX SQ Sequence 4 AA;

Query Match 100.0%; Score 25; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB ||||
1 GPRP 4

RESULT 18
ABU63154
ID ABU63154 standard; peptide; 4 AA.
XX AC
XX AC ABU63154;
XX DT 17-SEP-2003 (first entry)
XX DE Targeting ligand #4 used in novel diagnostic ultrasound method.
XX KW Ultrasound method; targeted vesicle composition; targeting ligand;

ultrasound scanning; dual frequency ultrasound insonation; micelle; liposome; phospholipid; ultrasound energy; vesicle oscillation; reflected ultrasound signal; ultrasound diagnosis; echogenic thrombus; endothelial tissue; epithelial cell; tumour cell; myocardial cell; integrin; malignancy; inflammation; heart; diseased tissue; imaging; gastrointestinal region; lymphatic system.

Synthetic.

US6521211-B1.

18-FEB-2003.

03-FEB-1999; 99US-00243640.

07-JUN-1995; 95US-00497684.

01-MAY-1996; 95US-00640464.

06-JUN-1996; 95US-00660032.

06-FEB-1998; 98US-0073913P.

22-DEC-1998; 98US-00218660.

(BRIM) BRISTOL-MYERS SQUIBB MEDICAL IMAGING INC.

Unger EC, Wu Y;

WPI; 2003-531036/50.

Ultrasound diagnosis, by administering targeted vesicle composition with vesicles encapsulating gas, in combination with targeting ligand, to a patient, and scanning patient by dual frequency ultrasound insonation.

Disclosure; Col 49; 96pp; English.

The present invention relates to a novel ultrasound method which involves administering to a patient a targeted vesicle composition which comprises vesicles encapsulating a gas, in combination with a targeting ligand, and scanning the patient using dual frequency ultrasound insonation. The vesicles themselves comprise a lipid, protein or polymer, and are selected from liposomes and micelles. The vesicles may comprise a phospholipid selected from dioleoylphosphatidylcholine, dimyristoylphosphatidylcholine, dipalmitoylphosphatidylcholine, distearoylphosphatidylcholine, dipalmitoylphosphatidylethanolamine, dioleoylphosphatidylethanolamine, N-succinyl-dioleoylphosphatidylethanolamine, 1-hexadecyl-2-palmitoylglycerophosphoethanolamine and phosphatidic acids. The method of scanning involves exposing the patient to a first ultrasound energy having a first insonation frequency to cause the vesicle to oscillate, and then subsequently, while the vesicle is oscillating, exposing the patient to a second ultrasound energy having a second insonation frequency that is different from the first insonation frequency, and detecting the reflected ultrasound signal. The method is useful for ultrasound diagnosis, for detection of a thrombus or enhancement of thrombus (e.g. old or echogenic thrombus) and for detecting vesicles targeted to epithelial cells, tumour cells, myocardial cells, and endothelial tissue including integrins associated with malignancy or inflammation. The method is also useful for diagnosing the presence or absence of diseased tissue in a patient, and for imaging one or more regions of a patient, such as for providing images of the heart, gastrointestinal region or lymphatic systems. ABUS3151-ABUS3172 represent targeting ligands that may be used in the method of the present invention

Sequence 4 AA;

Query Match 100.0%; Score 25; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
|||
Db 1 GRRP 4

RESULT 19

AA15728

ID AAR15728 standard; protein; 5 AA.

XX AAR15728;

XX 24-JAN-1992 (first entry)

XX Anticoagulant (11).

XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.

XX Synthetic.

ADD32227

ID ADD32227 standard; peptide; 4 AA.

XX ADD32227;

XX 15-JAN-2004 (first entry)

XX Fibrin polymerisation inhibiting peptide seq id 2.

XX antirheumatic; antiinflammatory; antiarthritic; peptide therapy; proinflammatory; tetrapeptide; inflammation; synovial joint inflammation; rheumatoid arthritis; fibrinogen A alpha chain; fibrin polymerisation; human.

XX Synthetic.

XX Homo sapiens.

XX US2003109431-A1.

XX 12-JUN-2003.

XX 17-AUG-2001; 2001US-00931009.

XX 17-AUG-2001; 2001US-00931009.

XX (SMIT/) SMITH T H.

XX Smith TH;

XX WPI; 2003-829401/77.

XX Inducing proinflammatory effects in human synovial or fibroblast cells comprises using a specific tetrapeptide which can also identify a receptor to the tetrapeptide.

XX Claim 1; SEQ ID NO 2; 16pp; English.

XX The invention describes a method of inducing proinflammatory effects in synovial or fibroblast cells comprising exposing the cells to a specific tetrapeptide (GRRP) peptide (I). (I) is used for inducing proinflammatory effects in synovial or fibroblast cells. An analogue of (I) is used for treating or preventing inflammation of a synovial joint or rheumatoid arthritis in a subject. (II) is used to identify a receptor for (I) comprising exposing several fibroblastic cells or synovial cells to (I). (I) can identify, isolate and clone the cell receptor to which it binds. This is the amino acid sequence of a fibrin polymerisation inhibiting peptide derived from the human fibrinogen A alpha chain.

XX Sequence 4 AA;

Query Match 100.0%; Score 25; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
|||
Db 1 GRRP 4

RESULT 20

AA15728

ID AAR15728 standard; protein; 5 AA.

XX AAR15728;

XX 24-JAN-1992 (first entry)

XX Anticoagulant (11).

XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.

XX Synthetic.

PN EP456152-A.
 XX
 PD 13-NOV-1991.
 XX
 PF 06-MAY-1991; 91EP-00107307.
 XX
 PR 08-MAY-1990; 90DE-04014655.
 XX
 XX (BEHW) BEHRINGWERKE AG.
 XX
 XX Stuber W, Fickensche K;
 XX
 XX WPI; 1991-334142/46.
 XX
 XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 PT chains but not thrombin.
 XX
 XX Claim 5; Page 8; 8pp; German.
 XX
 XX The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 XX
 XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 21
 AAR15720
 ID AAR15720 standard; protein; 5 AA.
 XX
 AC AAR15720;
 XX
 DT 24-JAN-1992 (first entry)
 XX
 DE Anticoagulant (3).
 XX
 XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 XX
 XX Synthetic.
 XX
 XX EP456152-A.
 XX
 PD 13-NOV-1991.
 XX
 PF 06-MAY-1991; 91EP-00107307.
 XX
 PR 08-MAY-1990; 90DE-04014655.
 XX
 XX (BEHW) BEHRINGWERKE AG.
 XX
 XX Stuber W, Fickensche K;
 XX
 XX WPI; 1991-334142/46.
 XX
 XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 PT chains but not thrombin.
 XX
 XX Claim 5; Page 8; 8pp; German.
 XX
 XX The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 XX

SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 22
 AAR15725
 ID AAR15725 standard; protein; 5 AA.
 XX
 AC AAR15725;
 XX
 DT 24-JAN-1992 (first entry)
 XX
 DE Anticoagulant (8).
 XX
 XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 XX
 XX Synthetic.
 XX
 XX EP456152-A.
 XX
 PD 13-NOV-1991.
 XX
 PF 06-MAY-1991; 91EP-00107307.
 XX
 PR 08-MAY-1990; 90DE-04014655.
 XX
 XX (BEHW) BEHRINGWERKE AG.
 XX
 XX Stuber W, Fickensche K;
 XX
 XX WPI; 1991-334142/46.
 XX
 XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 PT chains but not thrombin.
 XX
 XX Claim 5; Page 8; 8pp; German.
 XX
 XX The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 XX
 XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 1 GPRP 4
 RESULT 23
 AAR15722
 ID AAR15722 standard; protein; 5 AA.
 XX
 AC AAR15722;
 XX
 DT 24-JAN-1992 (first entry)
 XX
 DE Anticoagulant (5).
 XX
 XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 XX
 XX Synthetic.
 XX

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XX FH Key Location/Qualifiers
XX FT Misc-difference 5
XX FT /label= G-NH2, G-NH(Ethyl), G-NH(Ethyl)2, G-NH(Butyl)
XX PN EP456152-A.
XX PD 13-NOV-1991.
XX PF 06-MAY-1991; 91EP-00107307.
XX PR 08-MAY-1990; 90DE-04014655.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Stuber W, Fickensche K;
XX DR WPI; 1991-334142/46.
XX PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
XX PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
XX PT chains but not thrombin.
XX PS Claim 5; Page 8; 8pp; German.
XX CC The peptides represented in AAR15718-33 are anticoagulants which are more
XX CC effective than previously known chemically similar cpds. They can be used
XX CC for therapeutic and diagnostic purposes
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 24
AAR15723
ID AAR15723 standard; protein; 5 AA.
XX AC AAR15723;
XX DT 24-JAN-1992 (first entry)
XX DE Anticoagulant (6).
XX KW Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
XX OS Synthetic.
XX PN EP456152-A.
XX PD 13-NOV-1991.
XX PF 06-MAY-1991; 91EP-00107307.
XX PR 08-MAY-1990; 90DE-04014655.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Stuber W, Fickensche K;
XX DR WPI; 1991-334142/46.
XX PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
XX PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
XX PT chains but not thrombin.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 5
XX FT /label= W-NH2, W-NH(Methyl)
XX PN EP456152-A.
XX PD 13-NOV-1991.
XX PF 06-MAY-1991; 91EP-00107307.
XX PR 08-MAY-1990; 90DE-04014655.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Stuber W, Fickensche K;
XX DR WPI; 1991-334142/46.
XX PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-

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PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
PT chains but not thrombin.
XX PS Claim 5; Page 8; 8pp; German.
XX CC The peptides represented in AAR15718-33 are anticoagulants which are more
XX CC effective than previously known chemically similar cpds. They can be used
XX CC for therapeutic and diagnostic purposes
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 25
AAR15721
ID AAR15721 standard; protein; 5 AA.
XX AC AAR15721;
XX DT 24-JAN-1992 (first entry)
XX DE Anticoagulant (4).
XX KW Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
XX OS Synthetic.
XX PN EP456152-A.
XX PD 13-NOV-1991.
XX PF 06-MAY-1991; 91EP-00107307.
XX PR 08-MAY-1990; 90DE-04014655.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Stuber W, Fickensche K;
XX DR WPI; 1991-334142/46.
XX PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
XX PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
XX PT chains but not thrombin.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 5
XX FT /label= W-NH2, W-NH(Methyl)
XX PN EP456152-A.
XX PD 13-NOV-1991.
XX PF 06-MAY-1991; 91EP-00107307.
XX PR 08-MAY-1990; 90DE-04014655.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Stuber W, Fickensche K;
XX DR WPI; 1991-334142/46.
XX PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
XX PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
XX PT chains but not thrombin.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 5
XX FT /label= W-NH2, W-NH(Methyl)
XX PN EP456152-A.
XX PD 13-NOV-1991.
XX PF 06-MAY-1991; 91EP-00107307.
XX PR 08-MAY-1990; 90DE-04014655.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Stuber W, Fickensche K;
XX DR WPI; 1991-334142/46.
XX PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-

```

AC AAR15726;
 XX
 DT 24-JAN-1992 (first entry)
 DE
 DE Anticoagulant (9).
 XX
 XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 KW Synthetic.
 XX
 OS EP456152-A.
 PN
 XX 13-NOV-1991.
 PD
 XX
 XX 06-MAY-1991; 91EP-00107307.
 PF
 XX 08-MAY-1990; 90DE-04014655.
 PR
 XX (BEHW) BEHRINGWERKE AG.
 XX
 XX Stuber W, Fickensche K;
 PI
 XX WPI; 1991-334142/46.
 DR
 XX
 XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 chains but not thrombin.
 PT
 PT
 XX Claim 5; Page 8; 8pp; German.
 PS
 XX The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 CC
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB
 1 GPRP 4

RESULT 27
 AAR15724
 ID AAR15724 standard; protein; 5 AA.
 XX
 AC AAR15724;
 XX
 DT 24-JAN-1992 (first entry)
 DE
 DE Anticoagulant (7).
 XX
 XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 KW Synthetic.
 XX
 OS EP456152-A.
 PN
 XX 13-NOV-1991.
 PD
 XX
 XX 06-MAY-1991; 91EP-00107307.
 PF
 XX 08-MAY-1990; 90DE-04014655.
 PR
 XX (BEHW) BEHRINGWERKE AG.
 XX
 XX Stuber W, Fickensche K;
 PI
 XX WPI; 1991-334142/46.
 DR
 XX

PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 chains but not thrombin.
 PT
 XX Claim 5; Page 8; 8pp; German.
 PS
 XX The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 CC
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB
 1 GPRP 4

RESULT 28
 AAR15727
 ID AAR15727 standard; protein; 5 AA.
 XX
 AC AAR15727;
 XX
 DT 24-JAN-1992 (first entry)
 DE
 DE Anticoagulant (10).
 XX
 XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 KW Synthetic.
 XX
 OS EP456152-A.
 PN
 XX 13-NOV-1991.
 PD
 XX
 XX 06-MAY-1991; 91EP-00107307.
 PF
 XX 08-MAY-1990; 90DE-04014655.
 PR
 XX (BEHW) BEHRINGWERKE AG.
 XX
 XX Stuber W, Fickensche K;
 PI
 XX WPI; 1991-334142/46.
 DR
 XX
 XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 chains but not thrombin.
 PT
 XX Claim 5; Page 8; 8pp; German.
 PS
 XX The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 CC
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB
 1 GPRP 4

RESULT 29
 AAR15719
 ID AAR15719 standard; protein; 5 AA.

XX AAR15719;
 XX AC
 XX DT 24-JAN-1992 (first entry)
 XX DE Anticoagulant (2).
 XX KW Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 5
 FT Misc-label= S-NH2, S-NH(Isopropyl)
 XX PN EP456152-A.
 XX PD 13-NOV-1991.
 XX PF 06-MAY-1991; 91EP-00107307.
 XX PR 08-MAY-1990; 90DE-04014655.
 XX PA (BEHW) BEHRINGWERKE AG.
 XX PI Stuber W, Fickensche K;
 XX DR WPI; 1991-334142/46.
 XX ID New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
 XX AC AAR60333;
 XX DT 07-MAR-1995 (first entry)
 XX DE Blood coagulation inhibiting peptide.
 XX KW Blood; fibrin; coagulation; inhibition; thrombin; fibrinogen.
 XX OS Synthetic.
 XX PN JP06179696-A.
 XX PD 28-JUN-1994.
 XX PF 19-MAR-1993; 93JP-00085678.
 XX PR 13-OCT-1992; 92JP-00300380.
 XX PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 XX PA (NIHA-) NIPPON HAM KK.
 XX DR WPI; 1994-245692/30.
 XX ID New blood coagulation inhibiting peptide(s) having fibrin-agglutination inhibitory activity - useful for the treatment and prevention of thrombosis.
 XX PS Claim 1; Page 2; 6pp; Japanese.
 XX CC The blood coagulation inhibiting peptide comprises L-form amino acids and has fibrin agglutination inhibiting activity. Such peptides (see AAR60327-R60335) were synthesised using a peptide synthesiser (Applied Biosystems Co., 430A) and purified by high pressure liquid chromatography. To 0.2 ml of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated for 1 minute at 37 deg. Celsius. 0.2 ml of thrombin solution was added and the IC50 was determined according to the method of Kawasaki et al. This peptide had an IC50 of 65 micromolar compared with a control peptide of Gly-Pro-Arg which registered an IC50 of 250 micromolar

XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 1 GPRP 4

RESULT 31
 AAR60333
 ID AAR60333 standard; peptide; 5 AA.
 XX AC AAR60333;
 XX DT 07-MAR-1995 (first entry)
 XX DE Blood coagulation inhibiting peptide.
 XX KW Blood; fibrin; coagulation; inhibition; thrombin; fibrinogen.
 XX OS Synthetic.
 XX PN JP06179696-A.
 XX PD 28-JUN-1994.
 XX PF 19-MAR-1993; 93JP-00085678.
 XX PR 13-OCT-1992; 92JP-00300380.
 XX PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 XX PA (NIHA-) NIPPON HAM KK.
 XX DR WPI; 1994-245692/30.
 XX ID New blood coagulation inhibiting peptide(s) having fibrin-agglutination inhibitory activity - useful for the treatment and prevention of thrombosis.
 XX PS Claim 1; Page 2; 6pp; Japanese.
 XX CC The blood coagulation inhibiting peptide comprises L-form amino acids and has fibrin agglutination inhibiting activity. Such peptides (see AAR60327-R60335) were synthesised using a peptide synthesiser (Applied Biosystems Co., 430A) and purified by high pressure liquid chromatography. To 0.2 ml of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated for 1 minute at 37 deg. Celsius. 0.2 ml of thrombin solution was added and the IC50 was determined according to the method of Kawasaki et al. This peptide had an IC50 of 65 micromolar compared with a control peptide of Gly-Pro-Arg which registered an IC50 of 250 micromolar

XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 1 GPRP 4

RESULT 30
 AAR15718
 ID AAR15718 standard; peptide; 5 AA.
 XX AC AAR15718;
 XX DT 24-JAN-1992 (first entry)
 XX DE Anticoagulant (1).
 XX KW Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 XX OS Synthetic.
 XX PN EP456152-A.
 XX PD 13-NOV-1991.
 XX PF 06-MAY-1991; 91EP-00107307.
 XX PR 08-MAY-1990; 90DE-04014655.
 XX PA (BEHW) BEHRINGWERKE AG.


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CC other known affinity isolation procedures in that only mild elution
XX buffers are required to recover the bound fibrinogen
XX
SQ Sequence 5 AA;
    Query Match      100.0%; Score 25; DB 2; Length 5;
    Best Local Similarity 100.0%; Pred. No. 1.4e+06;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPRP 4
   ||||
DB 1 GPRP 4

RESULT 36
AAW47188
IID AAW47188 standard; peptide; 5 AA.
XX AC
XX AC
XX DT
XX XX
DE DE
XX XX
KW KW
KK KK
OS OS
XX OS
XX OS
PN PN
PD PD
XX PF
XX PF
XX PR
XX PA
XX PA
XX PI
XX DR
XX DR
XX PT
XX PT
XX PT
XX PS
XX PS
XX PS
This peptide ligand is immobilised and used for the purification of
fibrinogen. Such immobilised peptide ligands can be used in affinity
purification strategies. The invention provides a process for
inactivating virus that may be present in an aqueous solution containing
a free biologically active protein. The process comprises contacting the
solution with an immobilised ligand that binds to the protein, subjecting
the bound protein to virus-inactivating treatment and releasing the bound
protein by elution. The ligand is immobilised by being covalently bound
to a chromatographic support. The process is used for identifying and
inactivating viruses in protein solutions especially thrombin solutions.
Binding the protein to a solid phase protects it from denaturation during
the virus-inactivating treatment

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XX      SQ      Sequence 5 AA;
Query Match      100.0%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
        ||||
Db       1 GPRP 4

RESULT 37

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XX (FIBR-) FIBREX MEDICAL RES & DEV GMBH.
 XX Petzelbauer P;
 XX WPI; 2002-557605/59.
 XX Peptides or proteins based on fibrin or fibrinogen sequences, useful for
 XX combating fibrin-mediated disorders such as inflammation, transplant
 XX rejection, arteriosclerosis and reperfusion damage.
 XX Claim 2; Page 34; 41pp; German.
 XX The present invention relates to peptides based on the alpha- and beta-
 XX chain sequences of fibrin/fibrinogen, which are capable of acting as
 XX fibrin antagonists. These are used for the therapy of local and
 XX generalised inflammation associated with infection, autoimmune reactions,
 XX rheumatic disease, immune system dysfunction or genetic disease, for the
 XX prevention and treatment of organ transplantation rejection reactions,
 XX arteriosclerosis, reperfusion trauma, thrombotic disease and increased
 XX fibrin deposition associated with aging, or for the transport of other
 XX medicaments to human or animal endothelial cells. They may also be
 XX effective against fibrin-mediated tumour growth, collagenosis or
 XX psoriasis. The present sequence is a peptide of the invention
 XX Sequence 5 AA;
 XX Query Match 100.0%; Score 25; DB 5; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 GPRP 4
 XX ||||
 XX Db 1 GPRP 4
 XX RESULT 40
 XX AAO18329
 XX ID AAO18329 standard; peptide; 5 AA.
 XX AC AAO18329;
 XX DT 11-OCT-2002 (first entry)
 XX DE Fibrinogen based therapeutic peptide #5.
 XX KW Fibrin; fibrinogen; antagonist; inflammation; autoimmune disease;
 XX KW rheumatic disease; organ transplantation; arteriosclerosis;
 XX KW reperfusion trauma; thrombosis; cancer; antiinflammatory; antibacterial;
 XX KW immunosuppressive; antirheumatic; antiarteriosclerotic; vasotropic;
 XX KW thrombolytic; anticoagulant; cytostatic; antipsoriatic.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 5
 XX FT /note= "linked to between 2 and 30 peptide residues"
 XX PN WO200248180-A2.
 XX PD 20-JUN-2002.
 XX PF 07-DEC-2001; 2001WO-AT000387.
 XX PR 12-DEC-2000; 2000AT-00002063.
 XX PA (FIBR-) FIBREX MEDICAL RES & DEV GMBH.
 XX PI Petzelbauer P;
 XX WPI; 2002-557605/59.
 XX Peptides or proteins based on fibrin or fibrinogen sequences, useful for

PT combating fibrin-mediated disorders such as inflammation, transplant
 PT rejection, arteriosclerosis and reperfusion damage.
 XX Claim 2; Page 36; 41pp; German.
 XX The present invention relates to peptides based on the alpha- and beta-
 XX chain sequences of fibrin/fibrinogen, which are capable of acting as
 XX fibrin antagonists. These are used for the therapy of local and
 XX generalised inflammation associated with infection, autoimmune reactions,
 XX rheumatic disease, immune system dysfunction or genetic disease, for the
 XX prevention and treatment of organ transplantation rejection reactions,
 XX arteriosclerosis, reperfusion trauma, thrombotic disease and increased
 XX fibrin deposition associated with aging, or for the transport of other
 XX medicaments to human or animal endothelial cells. They may also be
 XX effective against fibrin-mediated tumour growth, collagenosis or
 XX psoriasis. The present sequence is a peptide of the invention
 XX Sequence 5 AA;
 XX Query Match 100.0%; Score 25; DB 5; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 GPRP 4
 XX ||||
 XX Db 1 GPRP 4
 XX RESULT 41
 XX AAR15733
 XX ID AAR15733 standard; protein; 6 AA.
 XX AC AAR15733;
 XX DT 24-JAN-1992 (first entry)
 XX DE Anticoagulant (16).
 XX KW Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 6
 XX FT /label= P-NH2, P-NH(Isopropyl)
 XX PN EP456152-A.
 XX PD 13-NOV-1991.
 XX PF 06-MAY-1991; 91EP-00107307.
 XX PR 08-MAY-1990; 90DE-04014655.
 XX PA (BEHW) BEHRINGWERKE AG.
 XX PI Stuber W, Fickensche K;
 XX WPI; 1991-334142/46.
 XX PT New anticoagulant penta- and hexa-peptide(s) - are Glycine-Proline-
 XX Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 XX chains but not thrombin.
 XX PS Claim 5; Page 8; 8pp; German.
 XX CC The peptides represented in AAR15718-33 are anticoagulants which are more
 XX effective than previously known chemically similar cpds. They can be used
 XX for therapeutic and diagnostic purposes
 XX Sequence 6 AA;
 XX Query Match 100.0%; Score 25; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 42
AAR15730
ID AAR15730 standard; protein; 6 AA.
AC AAR15730;
XX 24-JAN-1992 (first entry)
XX Anticoagulant (13).
XX Anticoagulant (13).
XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 6 /label= P-NH2, P-NH(Isopropyl)
FT
PN EP456152-A.
XX
XX 13-NOV-1991.
XX
XX 06-MAY-1991; 91EP-00107307.
XX
XX 08-MAY-1990; 90DE-04014655.
XX (BEHW) BEHRINGWERKE AG.
XX Stuber W, Fickensche K;
XX WPI; 1991-334142/46.
XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
XX Claim 5; Page 8; 8pp; German.
XX The peptides represented in AAR15718-33 are anticoagulants which are more effective than previously known chemically similar cpds. They can be used for therapeutic and diagnostic purposes
XX Sequence 6 AA;
PN EP456152-A.
XX
XX 13-NOV-1991.
XX
XX 06-MAY-1991; 91EP-00107307.
XX
XX 08-MAY-1990; 90DE-04014655.
XX (BEHW) BEHRINGWERKE AG.
XX Stuber W, Fickensche K;
XX WPI; 1991-334142/46.
XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
XX Claim 5; Page 8; 8pp; German.
XX The peptides represented in AAR15718-33 are anticoagulants which are more effective than previously known chemically similar cpds. They can be used for therapeutic and diagnostic purposes
XX Sequence 6 AA;
QY 1 GPRP 4
Db 1 GPRP 4

Query Match 100.0%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 43
AAR15731
ID AAR15731 standard; protein; 6 AA.
AC AAR15731;
XX
XX 24-JAN-1992 (first entry)
XX Anticoagulant (14).
XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
XX

OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 6 /label= P-NH2, P-NH(Isopropyl)
FT
PN EP456152-A.
XX
XX 13-NOV-1991.
XX
XX 06-MAY-1991; 91EP-00107307.
XX
XX 08-MAY-1990; 90DE-04014655.
XX (BEHW) BEHRINGWERKE AG.
XX Stuber W, Fickensche K;
XX WPI; 1991-334142/46.
XX New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
XX Claim 5; Page 8; 8pp; German.
XX The peptides represented in AAR15718-33 are anticoagulants which are more effective than previously known chemically similar cpds. They can be used for therapeutic and diagnostic purposes
XX Sequence 6 AA;
QY 1 GPRP 4
Db 1 GPRP 4

Query Match 100.0%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 44
AAR15732
ID AAR15732 standard; protein; 6 AA.
XX
XX AAR15732;
XX
XX 24-JAN-1992 (first entry)
XX Anticoagulant (15).
XX Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 6 /label= P-NH2, P-NH(Isopropyl)
FT
PN EP456152-A.
XX
XX 13-NOV-1991.
XX
XX 06-MAY-1991; 91EP-00107307.
XX
XX 08-MAY-1990; 90DE-04014655.
XX (BEHW) BEHRINGWERKE AG.
XX Stuber W, Fickensche K;
XX WPI; 1991-334142/46.

PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 PT chains but not thrombin.
 XX
 XX
 PS Claim 5; Page 8; 8pp; German.
 XX
 CC The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 XX
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 25; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 45
 AAR15729
 ID AAR15729 standard; protein; 6 AA.
 XX
 AC AAR15729;
 XX
 DT 24-JAN-1992 (first entry)
 XX
 DE Anticoagulant (12).
 XX
 KW Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 6 /label= P-NH2, P-NH(Isopropyl)
 FT
 PN EP456152-A.
 XX
 XX 13-NOV-1991.
 PD
 XX 06-MAY-1991; 91EP-00107307.
 PF
 XX 08-MAY-1990; 90DE-04014655.
 PR
 XX (BEHW) BEHRINGWERKE AG.
 PA
 XX Stuber W, Fickensche K;
 PI
 XX WPI; 1991-334142/46.
 DR
 XX
 XX
 PT New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
 PT Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
 PT chains but not thrombin.
 XX
 XX
 PS Claim 5; Page 8; 8pp; German.
 XX
 CC The peptides represented in AAR15718-33 are anticoagulants which are more
 CC effective than previously known chemically similar cpds. They can be used
 CC for therapeutic and diagnostic purposes
 XX
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 25; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 46
 AAR60332
 ID AAR60332 standard; peptide; 6 AA.
 XX
 AC AAR60332;
 XX
 DT 07-MAR-1995 (first entry)
 XX
 DE Blood coagulation inhibiting peptide.
 XX
 KW Blood; fibrin; coagulation; inhibition; thrombin; fibrinogen.
 XX
 OS Synthetic.
 XX
 PN JP06179696-A.
 XX
 PD 28-JUN-1994.
 XX
 PF 19-MAR-1993; 93JP-00085678.
 XX
 PR 13-OCT-1992; 92JP-00300380.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 DR WPI; 1994-245692/30.
 XX
 XX New blood coagulation inhibiting peptide(s) having fibrin-agglutination
 PT inhibitory activity - useful for the treatment and prevention of
 PT thrombosis.
 XX
 PS Claim 1; Page 2; 6pp; Japanese.
 XX
 CC The blood coagulation inhibiting peptide comprises L-form amino acids and
 CC has fibrin agglutination inhibiting activity. Such peptides (see AAR60327
 CC -R60335) were synthesised using a peptide synthesiser (Applied Biosystems
 CC Co., 430A) and purified by high pressure liquid chromatography. To 0.2 ml
 CC of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was
 CC added and incubated for 1 minute at 37 deg. Celsius. 0.2 ml of thrombin
 CC solution was added and the IC50 was determined according to the method of
 CC Kawasaki et al. This peptide had an IC50 of 70 micromolar compared with a
 CC control peptide of Gly-Pro-Arg which registered an IC50 of 250 micromolar
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 25; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 47
 AAY78985
 ID AAY78985 standard; peptide; 6 AA.
 XX
 AC AAY78985;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Tc-99m labelled fibrin-alpha-chain derived peptide.
 XX
 KW Fibrin-alpha-chain; Tc-99m thrombus detection; deep venous thrombosis;
 KW DVT; pulmonary embolism; PE; cell image; technetium-99m.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /label= 4Abu
 FT

/note= "The C-terminal has a Tc-99m-complexed peptide of formula NH₂-Gly-Ala-Gly-CO-NH- condensed onto it"

PT WO200009076-A2.
 XX
 XX
 PD 24-FEB-2000.
 XX
 XX
 PF 17-AUG-1999; 99WO-US019011.
 XX
 XX
 PR 17-AUG-1998; 98US-0096803P.
 XX
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 XX
 PI Thakur ML;
 XX
 XX
 DR WPI; 2000-205862/18.
 XX
 XX
 PT Method of imaging cells or tissues such as thrombus, particularly deep
 PT venous thrombosis and pulmonary embolism comprising using novel
 PT radiolabeled fibrin-alpha-chain peptides.
 XX
 XX
 PS Claim 5; Page 20; 29pp; English.
 XX
 XX
 CC This sequence represents a fibrin-alpha-chain derived peptide which is
 CC labelled with Technetium-99m (Tc-99m). This peptide is used in the
 CC composition of the invention which comprises a radiolabelled agent used
 CC for imaging mammalian tissue or cells. The composition is administered to
 CC a mammal at a target site, the radiolabelled moiety binds to fibrin and
 CC can be detected to show sites of thrombus. The composition is used to
 CC image mammalian cells or tissues, preferably thrombus, particularly deep
 CC venous thrombosis (DVT) and pulmonary embolism (PE)
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 25; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4
 RESULT 48
 ADE86867
 ID ADE86867 standard; peptide; 6 AA.
 XX
 XX
 AC ADE86867;
 XX
 XX
 DT 29-JAN-2004 (first entry)
 DE
 DE Fibrinogen binding peptide.
 XX
 XX
 KW ligand; target; matrix; binding characteristic; isoform; enantiomer;
 KW modification; FVIII; factor VIII; vWF; von Willebrand's factor.
 XX
 OS Synthetic.
 XX
 XX
 PN WO2003089922-A1.
 XX
 XX
 PD 30-OCT-2003.
 XX
 XX
 PF 14-APR-2003; 2003WO-US011799.
 XX
 XX
 PR 15-APR-2002; 2002US-0372091P.
 XX
 XX
 PA (AMNA-) AMERICAN NAT RED CROSS.
 XX
 XX
 PI Hammond DJ, Lathrop JT;
 XX
 XX
 DR WPI; 2004-022589/02.
 XX
 XX
 PT Characterizing a target that binds to a ligand, useful in concentrating

or separating target molecules form a sample comprises transferring a portion of the target of least one target-ligand-support complex to a second matrix.

Example 6; Page 19; 39pp; English.

This sequence represents a ligand which binds fibrinogen. This ligand was identified using the method of the invention for characterizing a target that binds to a ligand. The method comprises transferring at least a portion of the target of at least one target-ligand-support complex to a second matrix, where the position of the target within the second matrix corresponds to the position of the ligand-support complex within the first matrix, and detecting the target on the second matrix. The support used for the method is a resin bead. The method is useful in detecting a target that binds to a ligand or in determining preferred conditions under which a target or any molecule is transferred to the second matrix. It also provides a means to study the binding characteristics of the target and/or ligand. The method is also useful in separating isoforms and enantiomers from a sample. Detecting target-ligand binding of the invention avoids modification of the target for detection, enables detection of a target separated from a ligand and identification of the ligand, and allows detection of the target via its biological, biochemical or chemical activity compared to currently available detection techniques which have potential drawbacks, namely modification of the target through radiolabel attachment, interference from ligand-target-detection system interactions, and the ability to detect only a limited number of targets for which detection systems already exist.

Sequence 6 AA;

Query Match 100.0%; Score 25; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 49
 ADD69979
 ID ADD69979 standard; peptide; 7 AA.

XX
 XX
 AC ADD69979;
 XX
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX
 DE
 DE Primate neural cell production method-related MEDII peptide #1.

XX
 KW Primate neural cell; pluripotent primate cell; MEDII; neural disease;
 KW Parkinson's disease; Huntington's disease; lysosomal storage disease;
 KW multiple sclerosis; memory disorder; behavioural disorder;
 KW Alzheimer's disease; macular degeneration; toxicity testing;
 KW proline-containing peptide.

XX Unidentified.

XX WO2003078585-A2.

XX PD 25-SEP-2003.

XX PF 13-MAR-2003; 2003WO-US007665.

XX PR 13-MAR-2002; 2002US-0364381P.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX (BRES-) BRESAGEN LTD.

XX Stice S, Calhoun J, Lyons I, Mitalipova M, Robins A;

XX WPI; 2003-779126/73.

XX Producing a primate neural cell, useful for treating Parkinson's disease,

PT Alzheimer's disease, Huntington's disease, or macular degeneration,
PT comprises culturing a pluripotent primate cell with a MEDII conditioned
PT medium.

XX
XX
PS Disclosure; SEQ ID NO 1; 36pp; English.

CC The invention comprises a method for producing a primate neural cell, the
CC method involves culturing a pluripotent primate cell with a MEDII
CC conditioned medium. The method and the primate neural cell of the
CC invention are useful for treating a neural disease, such as: Parkinson's
CC disease, Huntington's disease, lysosomal storage diseases, multiple
CC sclerosis, memory and behavioural disorders, Alzheimer's disease, and
CC macular degeneration. The neural cells are also useful for testing the
CC effect of molecules on neural differentiation or survival, in toxicity
CC testing or in testing molecules for their effects on neural or neuronal
CC functions. The present amino acid sequence represents a proline-
CC containing peptide that may be used in the MEDII conditioned medium in
CC the method of the invention.

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 25; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 4 GPRP 7

RESULT 50

AAR69319
ID AAR69319 standard; peptide; 8 AA.

AC AAR69319;

DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)

DE Gp IIB/IIIA receptor ligand used in scintigraphic imaging of thrombi.

KW Scintigraphy; thrombus; thrombi; imaging; specific binding;
KW technetium-99m; radiolabelled; Gp IIB/IIIA receptor ligand.

XX Synthetic.

EH Key Location/Qualifiers
FT Modified-site 5 /note= "S-acetamidomethyl-Cys"
FT Modified-site 7
FT Modified-site 8 /note= "S-acetamidomethyl-Cys"
FT Modified-site 8 /note= "this residue is joined via the SH group to tris(2
FT -succinimidomethyl)amine (TSEA) to form one of three such
FT peptides connected to the amine; i.e. forming a product
FT of formula (peptide)3-TSEA"

XX WO9323085-A1.

XX 25-NOV-1993.

XX 21-MAY-1993; 93WO-US004794.

XX 21-MAY-1992; 92US-00886752.

XX (DIAT-) DIATECH INC.

XX Dean RT, Lister-James J;

XX WPI; 1993-386229/48.

XX Reagent for scintigraphic imaging of thrombi with 99m technetium -
PT comprises synthetic peptide which binds to thrombus covalently coupled to

PT metal binding gp., rapidly cleared from blood and tissue.

XX Claim 19; Page 42; 6pp; English.

CC The invention relates to reagents for scintigraphic imaging of a thrombus
CC in-vivo, comprising (A) a specific binding compound capable of binding to
CC at least one component of a thrombus, covalently linked to (B) a
CC technetium-99m-binding moiety. Specific peptides constituting the
CC reagents are claimed as new. The present peptide is one such peptide, in
CC which the Cys(acyl)-Gly-Cys(acyl) moiety is the 99m-Tc binding moiety and
CC the residue constitutes the thrombus-binding component. (Updated on 25-
CC MAR-2003 to correct PN field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 25; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

Search completed: September 7, 2004, 18:58:18
Job time : 127 secs

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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:25:22 ; Search time 122 Seconds

(without alignments)
10.330 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 7583

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Published Applications AA:

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	4	9	US-09-779-054-16
2	25	100.0	4	10	US-09-931-009A-2
3	25	100.0	4	14	US-10-046-801-6
4	25	100.0	4	15	US-10-016-569A-25
5	25	100.0	4	15	US-10-308-544-25
6	19	76.0	4	12	US-10-243-613-101
7	19	76.0	4	12	US-10-275-427A-34
8	19	76.0	4	14	US-10-211-088-115
9	18	72.0	4	9	US-09-040-518-8
10	18	72.0	4	9	US-09-804-733A-24
11	18	72.0	4	9	US-08-785-614B-30
12	18	72.0	4	9	US-09-925-715-26
13	18	72.0	4	11	US-09-807-742-3
14	18	72.0	4	12	US-10-619-520-3
15	18	72.0	4	12	US-10-619-520-4

ALIGNMENTS

RESULT 1
US-09-779-054-16
; Sequence 16, Application US/09779054
; Patent No. US20020120102A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Xinjie
; APPLICANT: Kakkar, Vijay
; TITLE OF INVENTION: USE OF DENDROSPIN AS A SCAFFOLD FOR NON-DENDROSPIN DOMAINS
; FILE REFERENCE: A-70312/TAL/AMS
; CURRENT APPLICATION NUMBER: US/09/779,054
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: GB 0002625.2
; PRIOR FILING DATE: 2000-02-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT

16	18	72.0	4	12	US-10-619-520-5	Sequence 5, Appl
17	18	72.0	4	14	US-10-158-742A-19	Sequence 19, Appl
18	18	72.0	4	14	US-10-028-075B-151	Sequence 151, Appl
19	18	72.0	4	14	US-10-029-206A-151	Sequence 151, Appl
20	18	72.0	4	15	US-10-395-073-1	Sequence 1, Appl
21	18	72.0	4	15	US-10-342-331-14	Sequence 14, Appl
22	18	72.0	4	16	US-10-722-075-30	Sequence 30, Appl
23	17	68.0	4	12	US-10-276-608-9	Sequence 9, Appl
24	17	68.0	4	12	US-10-276-608-11	Sequence 11, Appl
25	17	68.0	4	14	US-10-198-677-57	Sequence 57, Appl
26	17	68.0	4	14	US-10-198-677-59	Sequence 59, Appl
27	16	64.0	4	9	US-09-922-091-11	Sequence 11, Appl
28	16	64.0	4	9	US-09-938-112-11	Sequence 11, Appl
29	16	64.0	4	12	US-10-154-332-2	Sequence 2, Appl
30	16	64.0	4	14	US-10-082-691-11	Sequence 11, Appl
31	16	64.0	4	15	US-10-376-121A-133	Sequence 133, Appl
32	16	64.0	4	16	US-10-250-508-30	Sequence 30, Appl
33	14	56.0	4	10	US-09-852-910-158	Sequence 158, Appl
34	14	56.0	4	12	US-10-276-608-10	Sequence 10, Appl
35	14	56.0	4	12	US-10-276-608-12	Sequence 12, Appl
36	14	56.0	4	13	US-10-146-221-20	Sequence 20, Appl
37	14	56.0	4	14	US-10-096-986-7	Sequence 7, Appl
38	14	56.0	4	14	US-10-198-677-56	Sequence 56, Appl
39	14	56.0	4	14	US-10-198-677-58	Sequence 58, Appl
40	14	56.0	4	15	US-10-411-336A-158	Sequence 158, Appl
41	14	56.0	4	16	US-10-299-636-110	Sequence 110, Appl
42	14	56.0	4	16	US-10-293-636-111	Sequence 111, Appl
43	14	56.0	4	16	US-10-778-253-36	Sequence 36, Appl
44	13	52.0	2	10	US-09-836-433-15	Sequence 15, Appl
45	13	52.0	3	9	US-09-967-003-1	Sequence 1, Appl
46	13	52.0	3	10	US-09-836-433-16	Sequence 16, Appl
47	13	52.0	3	10	US-09-755-630A-277	Sequence 277, Appl
48	13	52.0	3	12	US-10-345-198-64	Sequence 64, Appl
49	13	52.0	3	12	US-10-363-208-192	Sequence 192, Appl
50	13	52.0	3	12	US-10-232-838-3	Sequence 3, Appl
51	13	52.0	3	14	US-10-283-838-1	Sequence 1, Appl
52	13	52.0	3	16	US-10-320-731A-26	Sequence 26, Appl
53	13	52.0	4	9	US-09-848-834A-5	Sequence 5, Appl
54	13	52.0	4	9	US-09-256-650-4	Sequence 4, Appl
55	13	52.0	4	9	US-09-269-439-10	Sequence 10, Appl
56	13	52.0	4	9	US-09-269-439-11	Sequence 11, Appl
57	13	52.0	4	9	US-09-908-322-71	Sequence 71, Appl
58	13	52.0	4	9	US-09-916-940-3	Sequence 3, Appl
59	13	52.0	4	9	US-09-825-561A-70	Sequence 70, Appl
60	13	52.0	4	9	US-09-947-387-12	Sequence 12, Appl
61	13	52.0	4	9	US-09-957-995A-14	Sequence 14, Appl
62	13	52.0	4	9	US-09-972-772-26	Sequence 26, Appl
63	13	52.0	4	9	US-09-972-772-27	Sequence 27, Appl
64	13	52.0	4	10	US-09-836-433-17	Sequence 17, Appl
65	13	52.0	4	10	US-09-783-931-71	Sequence 71, Appl

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: thrombin-binding sequence
US-09-779-054-16

Query Match 100.0%; Score 25; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 2
US-09-931-009A-2
; Sequence 2, Application US/09931009A
; Publication No. US20030109431A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Theresa H.
; TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
; FILE REFERENCE: US 1257/01 (VA)
; CURRENT APPLICATION NUMBER: US/09/931,009A
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown. Obtained from a commercial source.
US-09-931-009A-2

Query Match 100.0%; Score 25; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 3
US-10-046-801-6
; Sequence 6, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGRI592
; CURRENT APPLICATION NUMBER: US/10/046,801
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1e1 Sequence
US-10-046-801-6

Query Match 100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 4
US-10-016-569A-25
; Sequence 25, Application US/10016569A
; Publication No. US20030229013A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Iu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; TITLE OF INVENTION: the Same
; FILE REFERENCE: PI379
; CURRENT APPLICATION NUMBER: US/10/016,569A
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
; OTHER INFORMATION: US-10-016-569A-25

Query Match 100.0%; Score 25; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 5
US-10-308-644-25
; Sequence 25, Application US/10308644
; Publication No. US20030229017A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Iu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: PI379
; CURRENT APPLICATION NUMBER: US/10/308,644
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
; OTHER INFORMATION: US-10-308-644-25

Query Match 100.0%; Score 25; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 6
US-10-243-613-101
; Sequence 101, Application US/10243613
; Publication No. US20040053823A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Jeffrey W.

; APPLICANT: Chen, Emily I.
; APPLICANT: Kridel, Steven J.
; TITLE OF INVENTION: Selective Substrates for Matrix
; TITLE OF INVENTION: Metalloproteases
; FILE REFERENCE: P-LJ 5432
; CURRENT APPLICATION NUMBER: US/10/243,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/953,592
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-243-613-101

Query Match 76.0%; Score 19; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
Db 1 PRP 3

RESULT 7
US-10-275-427A-34
; Sequence 34, Application US/10275427A
; Publication No. US20040072319A1
; GENERAL INFORMATION:
; APPLICANT: Nash et al.
; TITLE OF INVENTION: Molecules that Modulate Ubiquitin-Dependent Proteolysis and
; TITLE OF INVENTION: Methods for Identifying Same
; FILE REFERENCE: WTSI-P01-011
; CURRENT APPLICATION NUMBER: US/10/275,427A
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/CA01/00632
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDP Peptide
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: PHOSPHORYLATION
US-10-275-427A-34

Query Match 76.0%; Score 19; DB 12; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPTP 4

RESULT 8
US-10-211-088-115
; Sequence 115, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: NO. US20030104479A1el Fusion Proteins And Assays For Molecular Bi

; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-115

Query Match 76.0%; Score 19; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
Db 2 PRP 4

RESULT 9
US-09-040-518-8
; Sequence 8, Application US/09040518
; Patent No. US20010042255A1
; GENERAL INFORMATION:
; APPLICANT: Karatzas, Costas N.
; TITLE OF INVENTION: PRODUCTION OF BIOFILAMENTS IN TRANSGENIC
; TITLE OF INVENTION: ANIMALS
; FILE REFERENCE: 06632/011001
; CURRENT APPLICATION NUMBER: US/09/040,518
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed peptide to act as a recognition site for
; OTHER INFORMATION: an enzyme
US-09-040-518-8

Query Match 72.0%; Score 18; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 2 GPR 4

RESULT 10
US-09-804-733A-24
; Sequence 24, Application US/09804733A
; Patent No. US20020059656A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING REPEATING UNITS
; FILE REFERENCE: MTC6614.2
; CURRENT APPLICATION NUMBER: US/09/804,733A
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/188,990
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 4

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT

; LOCATION: (1)..(4)
; OTHER INFORMATION: Trypsin cleavage site
US-09-804-733A-24

Query Match 72.0%; Score 18; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
Db 2 GPR 4

RESULT 11

US-09-765-614B-30
; Sequence 30, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nvcomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Thrombus
; OTHER INFORMATION: Binding peptide
US-09-765-614B-30

Query Match 72.0%; Score 18; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
Db 1 GPR 3

RESULT 12

US-09-925-715-26
; Sequence 26, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nvcomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Thrombus
; OTHER INFORMATION: binding peptide
US-09-925-715-26

Query Match 72.0%; Score 18; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
Db 1 GPR 3

RESULT 13

US-09-807-742-3
; Sequence 3, Application US/09807742
; Publication No. US20030204864A1
; GENERAL INFORMATION:
; APPLICANT: DANIELL, HENRY
; TITLE OF INVENTION: PRODUCTION OF PHARMACEUTICAL PROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLASTIDS
; FILE REFERENCE: 1465-PCT-US-00
; CURRENT APPLICATION NUMBER: US/09/807,742
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/06288
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-09-807-742-3

Query Match 72.0%; Score 18; DB 11; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPGP 4

RESULT 14

US-10-619-520-3
; Sequence 3, Application US/10619520
; Publication No. US20040057957A1
; GENERAL INFORMATION:
; APPLICANT: Robert, Koll
; APPLICANT: Richter, W.
; APPLICANT: Tschoppe, W.
; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
; FILE REFERENCE: Attorney Docket No. US20040057957A1 1328/2
; CURRENT APPLICATION NUMBER: US/10/619,520
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; OTHER INFORMATION: X is any amino acid
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Synthesized Peptide
US-10-619-520-3

Query Match 72.0%; Score 18; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 15
US-10-619-520-4
; Sequence 4, Application US/10619520
; Publication No. US20040057957A1
; GENERAL INFORMATION:
; APPLICANT: Robert, Koll
; APPLICANT: Richter, W.
; APPLICANT: Bieber, Franz
; APPLICANT: Tschoepe, W.
; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DI
; FILE REFERENCE: Attorney Docket No. US20040057957A1 1328/2
; CURRENT APPLICATION NUMBER: US/10/619,520
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Synthesized Peptide
US-10-619-520-4

Query Match 72.0%; Score 18; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 16
US-10-619-520-5
; Sequence 5, Application US/10619520
; Publication No. US20040057957A1
; GENERAL INFORMATION:
; APPLICANT: Robert, Koll
; APPLICANT: Richter, W.
; APPLICANT: Bieber, Franz
; APPLICANT: Tschoepe, W.
; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DI
; FILE REFERENCE: Attorney Docket No. US20040057957A1 1328/2
; CURRENT APPLICATION NUMBER: US/10/619,520
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Synthesized Peptide
US-10-619-520-5

Query Match 72.0%; Score 18; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 1 GPR 3

RESULT 17
US-10-158-742A-19
; Sequence 19, Application US/10158742A
; Publication No. US20030104581A1
; GENERAL INFORMATION:
; APPLICANT: Hoess, Eva
; APPLICANT: Meier, Thomas
; APPLICANT: Pestlin, Gabriele
; APPLICANT: Popp, Friedrich
; APPLICANT: Reichert, Klaus
; APPLICANT: Schmuck, Rainer
; APPLICANT: Schneidinger, Bernd
; APPLICANT: Seidel, Christoph
; APPLICANT: Tischer, Wilhelm
; TITLE OF INVENTION: PROCESS FOR MAKING ANTIFUSOGENIC FUSION PEPTIDES THAT FORM
; FILE REFERENCE: 20904
; CURRENT APPLICATION NUMBER: US/10/158,742A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: EP 01114497.9
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE:
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cleavage
; OTHER INFORMATION: sequence
US-10-158-742A-19

Query Match 72.0%; Score 18; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 2 GPR 4

RESULT 18
US-10-028-075B-151
; Sequence 151, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 151
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sprembl/09UCG8/09UCG8
US-10-028-075B-151

Query Match 72.0%; Score 18; DB 14; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

Qy 1 GPR 3
|||
Db 2 GPR 4

RESULT 19

US-10-029-206A-151
; Sequence 151, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 151
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sprembl/Q9UCG8/Q9UCG8
US-10-029-206A-151

Query Match 72.0%; Score 18; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
|||
Db 2 GPR 4

RESULT 20

US-10-396-073-1
; Sequence 1, Application US/10396073
; Publication No. US20030207330A1
; GENERAL INFORMATION:
; APPLICANT: Wescott, Charles R.
; APPLICANT: Sato, Aaron K.
; TITLE OF INVENTION: FIBRINOGEN BINDING MOIETIES
; FILE REFERENCE: DYX-036.1 PCT; DYX-036.1 US
; CURRENT APPLICATION NUMBER: US/10/396,073
; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/367,645
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: N-terminal peptide of fibrinogen alpha chain
US-10-396-073-1

Query Match 72.0%; Score 18; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
|||
Db 1 GPR 3

RESULT 21

US-10-342-331-14
; Sequence 14, Application US/10342331
; Publication No. US20030229205A1
; GENERAL INFORMATION:
; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOUWSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOOROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHELIE D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; TITLE OF INVENTION: PREPARATION THEREOF
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/10/342,331
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US/09/219,849
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-342-331-14

Query Match 72.0%; Score 18; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
|||
Db 2 GPR 4

RESULT 22

US-10-722-075-30
; Sequence 30, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Thrombus
; OTHER INFORMATION: binding peptide
US-10-722-075-30

Query Match 72.0%; Score 18; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
|||
Db 1 GPR 3

RESULT 23

US-10-276-608-9
; Sequence 9, Application US/10276608
; Publication No. US20040039175A1
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Demaison, Christophe
; APPLICANT: Moore, Michael
; APPLICANT: Papworth, Monika A
; APPLICANT: Reynolds, Lindsey
; APPLICANT: Ullman, Christopher G
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: SABI-035/00US (G13-US)
; CURRENT APPLICATION NUMBER: US/10/276,608
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: canonical linker
US-10-276-608-9

Query Match 68.0%; Score 17; DB 12; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
|
|
|
Db 1 GERP 4

RESULT 24

US-10-276-608-11
; Sequence 11, Application US/10276608
; Publication No. US20040039175A1
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Demaison, Christophe
; APPLICANT: Moore, Michael
; APPLICANT: Papworth, Monika A
; APPLICANT: Reynolds, Lindsey
; APPLICANT: Ullman, Christopher G
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: SABI-035/00US (G13-US)
; CURRENT APPLICATION NUMBER: US/10/276,608
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: canonical linker
US-10-276-608-11

Query Match 68.0%; Score 17; DB 12; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
|
|
|
Db 1 GORP 4

RESULT 25

US-10-276-608-11

US-10-198-677-57
; Sequence 57, Application US/10198677
; Publication No. US20030119023A1
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Moore, Michael
; TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 8325-2011 / G11-US1
; CURRENT APPLICATION NUMBER: US/10/198,677
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: canonical linker
; OTHER INFORMATION: sequence variant
US-10-198-677-57

Query Match 68.0%; Score 17; DB 14; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
|
|
|
Db 1 GERP 4

RESULT 26

US-10-198-677-59
; Sequence 59, Application US/10198677
; Publication No. US20030119023A1
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Moore, Michael
; TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 8325-2011 / G11-US1
; CURRENT APPLICATION NUMBER: US/10/198,677
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: canonical linker
; OTHER INFORMATION: sequence variant
US-10-198-677-59

Query Match 68.0%; Score 17; DB 14; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
|
|
|
Db 1 GERP 4

RESULT 27

US-09-922-093-11
; Sequence 11, Application US/09922093
; Patent No. US20020037833A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen

```
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875CIP2
; CURRENT APPLICATION NUMBER: US/09/922,093
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/625,098
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 09/489,667
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a naturally occurring am
; OTHER INFORMATION: ino thermal peptide fragment derived from substance P.
US-09-922-093-11

Query Match          64.0%; Score 16; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PRP 4
      |||
Db      2 PKP 4

RESULT 28
US-09-938-112-11
; Sequence 11, Application US/09938112
; Patent No. US2002008689A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875DIV
; CURRENT APPLICATION NUMBER: US/09/938,112
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 09/489,667
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a naturally occurring am
; OTHER INFORMATION: ino thermal peptide fragment derived from substance P.
US-09-938-112-11

Query Match          64.0%; Score 16; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PRP 4
      |||
Db      2 PKP 4

RESULT 29
US-10-154-332-2
; Sequence 2, Application US/10154332
; Publication No. US20030225010A1
; GENERAL INFORMATION:
; APPLICANT: Rameshwar, Pranela
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE REGULATION OF PROLIFERATIO
; FILE REFERENCE: 269/280
; CURRENT APPLICATION NUMBER: US/10/154,332
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a naturally occurring am
; OTHER INFORMATION: ino thermal peptide fragment derived from substance P.
US-09-938-112-11

Query Match          64.0%; Score 16; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PRP 4
      |||
Db      2 PKP 4

RESULT 30
US-10-082-691-11
; Sequence 11, Application US/10082691
; Publication No. US20030165541A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION PAIN
; FILE REFERENCE: D-3018
; CURRENT APPLICATION NUMBER: US/10/082,691
; CURRENT FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a
; OTHER INFORMATION: naturally occurring amino terminal peptide fragment
; OTHER INFORMATION: derived from substance P.
; NAME/KEY: MOD RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: This sequence is made up by the first four amino
; OTHER INFORMATION: acids of substance P.
; PUBLICATION INFORMATION:
; PATENT DOCUMENT NUMBER: 5891842
; PATENT FILING DATE: 1996-04-12
; PUBLICATION DATE: 1999-04-16
; PUBLICATION INFORMATION:
; JOURNAL: Nature
; VOLUME: 262
; PAGES: 784-785
; DATE: 1986
; PUBLICATION INFORMATION:
; JOURNAL: J. Neurosci.
; VOLUME: 10
; PAGES: 1309-1318
; DATE: 1990
; US-10-082-691-11

Query Match          64.0%; Score 16; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PRP 4
      |||
Db      2 PKP 4

RESULT 31
US-10-376-121A-133
; Sequence 133, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
```

```
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-332-2

Query Match          64.0%; Score 16; DB 12; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PRP 4
      |||
Db      2 PKP 4

RESULT 30
US-10-082-691-11
; Sequence 11, Application US/10082691
; Publication No. US20030165541A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION PAIN
; FILE REFERENCE: D-3018
; CURRENT APPLICATION NUMBER: US/10/082,691
; CURRENT FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a
; OTHER INFORMATION: naturally occurring amino terminal peptide fragment
; OTHER INFORMATION: derived from substance P.
; NAME/KEY: MOD RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: This sequence is made up by the first four amino
; OTHER INFORMATION: acids of substance P.
; PUBLICATION INFORMATION:
; PATENT DOCUMENT NUMBER: 5891842
; PATENT FILING DATE: 1996-04-12
; PUBLICATION DATE: 1999-04-16
; PUBLICATION INFORMATION:
; JOURNAL: Nature
; VOLUME: 262
; PAGES: 784-785
; DATE: 1986
; PUBLICATION INFORMATION:
; JOURNAL: J. Neurosci.
; VOLUME: 10
; PAGES: 1309-1318
; DATE: 1990
; US-10-082-691-11

Query Match          64.0%; Score 16; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PRP 4
      |||
Db      2 PKP 4

RESULT 31
US-10-376-121A-133
; Sequence 133, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
```

```

; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.125
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376.121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMFL114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-10-376-121A-133

Query Match 64.0%; Score 16; DB 15; Length 4;
Best Local Similarity 75.0%; Pred. NO. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRP 4
Db 1 GRRP 4

RESULT 32
US-10-250-508-30
; Sequence 30, Application US/10250508
; Publication No. US20040121327A1
; GENERAL INFORMATION:
; APPLICANT: Vanns, Michael
; APPLICANT: Strassburg, Christian
; TITLE OF INVENTION: Method for Predicting the Potential Risk of Carcinomas and
; FILE REFERENCE: 03100178aa
; CURRENT APPLICATION NUMBER: US/10/250,508
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/DE02/00003
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: DE 101 00 238.6
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: canonical linker

```

```

; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(4)
; OTHER INFORMATION: amino acid residues 7-10 of UGT1A1 as shown in Figure 4
US-10-250-508-30

Query Match 64.0%; Score 16; DB 16; Length 4;
Best Local Similarity 75.0%; Pred. NO. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRP 4
Db 1 GRRP 4

RESULT 33
US-09-852-910-158
; Sequence 158, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S;
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 158
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(4)
; OTHER INFORMATION: G alpha t library linker sequence
US-09-852-910-158

Query Match 56.0%; Score 14; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. NO. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 2 GPQ 4

RESULT 34
US-10-276-608-10
; Sequence 10, Application US/10276608
; Publication No. US20040039175A1
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Demaison, Christophe
; APPLICANT: Moore, Michael
; APPLICANT: Papworth, Monika A
; APPLICANT: Reynolds, Lindsey
; APPLICANT: Ullman, Christopher G
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
; FILE REFERENCE: SABI-035/00US (G13-US)
; CURRENT APPLICATION NUMBER: US/10/276,608
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: canonical linker

```

US-10-276-608-10

Query Match 56.0%; Score 14; DB 12; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPRP 4
| : |
Db 1 GEKP 4

RESULT 35

US-10-276-608-12
; Sequence 12, Application US/10276608
; Publication No. US20040039175A1
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Demaison, Christophe
; APPLICANT: Moore, Michael
; APPLICANT: Papworth, Monika A
; APPLICANT: Reynolds, Lindsey
; APPLICANT: Ullman, Christopher G
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: SABI-035/00US (G13-US)
; CURRENT APPLICATION NUMBER: US/10/276,608
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: canonical linker

Query Match 56.0%; Score 14; DB 12; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPRP 4
| : |
Db 1 GEKP 4

RESULT 36

US-10-146-221-20
; Sequence 20, Application US/10146221
; Publication No. US20020173006A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Poly Zinc Finger Proteins With Improved Linkers
; FILE REFERENCE: 019496-002510US
; CURRENT APPLICATION NUMBER: US/10/146,221
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/260,629
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic linker sequence

Query Match 56.0%; Score 14; DB 13; Length 4;

Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPRP 4
| : |
Db 1 GEKP 4

RESULT 37

US-10-096-986-7
; Sequence 7, Application US/10096986
; Publication No. US20030083464A1
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Richardson, Charles
; APPLICANT: Chambers, James
; APPLICANT: Causey, Stuart
; APPLICANT: Follock, Thomas J.
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W.
; TITLE OF INVENTION: No. US20030083464A1 Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,986
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,791
; FILING DATE: 22-No. US20030083464A1-1999
; APPLICATION NUMBER: US 08/482,085
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-096-986-7

Query Match 56.0%; Score 14; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRP 4
Db 1 PEP 3

RESULT 38
US-10-198-677-56
; Sequence 56, Application US/10198677
; Publication No. US20030119023A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: MOORE, Michael
; TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 8325-2011 / Gil-US1
; CURRENT APPLICATION NUMBER: US/10/198,677
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: canonical linker
; OTHER INFORMATION: sequence variant
US-10-198-677-56

Query Match 56.0%; Score 14; DB 14; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GERP 4

RESULT 39
US-10-198-677-58
; Sequence 58, Application US/10198677
; Publication No. US20030119023A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: MOORE, Michael
; TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 8325-2011 / Gil-US1
; CURRENT APPLICATION NUMBER: US/10/198,677
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: canonical linker
; OTHER INFORMATION: sequence variant
US-10-198-677-58

Query Match 56.0%; Score 14; DB 14; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GERP 4

RESULT 40
US-10-411-336A-158
; Sequence 158, Application US/10411336A
; Publication No. US20040018558A1
; GENERAL INFORMATION:
; APPLICANT: GILCHRIST, ANNETTE
; APPLICANT: HAMM, HEIDI
; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: SIGNALING
; FILE REFERENCE: 2661-102
; CURRENT APPLICATION NUMBER: US/10/411,336A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/852910
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/275472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G alpha t library linker sequence
US-10-411-336A-158

Query Match 56.0%; Score 14; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
Db 2 GPQ 4

RESULT 41
US-10-299-636-110
; Sequence 110, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 110
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-110

Query Match 56.0%; Score 14; DB 16; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRP 4
Db 1 PEP 3

RESULT 42
US-10-299-636-111
; Sequence 111, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57903/361
; CURRENT APPLICATION NUMBER: US/10/299, 636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-111

Query Match 56.0%; Score 14; DB 16; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
QY 2 PRP 4
DB 1 FEP 3

RESULT 43
US-10-778-253-36
; Sequence 36, Application US/10778253
; Publication No. US20040162232A1
; GENERAL INFORMATION:
; APPLICANT: Health Matrix Sciences
; APPLICANT: Mitts, Thomas
; APPLICANT: Jimenez, Felipe
; TITLE OF INVENTION: ELASTIN DIGEST COMPOSITIONS AND METHODS UTILIZING SAME
; FILE REFERENCE: 126595.101
; CURRENT APPLICATION NUMBER: US/10/778,253
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447461
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 4
; TYPE: PRT
; ORGANISM: BOVINE
US-10-778-253-36

Query Match 56.0%; Score 14; DB 16; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPR 3
DB 1 GPQ 3

RESULT 44
US-09-836-433-15
; Sequence 15, Application US/09836433
; Publication No. US20030049797A1

; GENERAL INFORMATION:
; APPLICANT: Yuki, Yoshikazu
; APPLICANT: Udaaka, Shigezo
; TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
; FILE REFERENCE: No. US20030049797A1 Assigned
; CURRENT APPLICATION NUMBER: US/09/836,433
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 2
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-836-433-15

Query Match 52.0%; Score 13; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GP 2
DB 1 GP 2

RESULT 45
US-09-967-003-1
; Sequence 1, Application US/09967003
; Patent No. US20020107202A1
; GENERAL INFORMATION:
; APPLICANT: Haddox, Jeffrey
; APPLICANT: Pfister, Robert
; APPLICANT: Blalock, James
; APPLICANT: Matteo, Villain
; TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 92750/57
; CURRENT APPLICATION NUMBER: US/09/967,003
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/521,365
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US 60/123,409
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3
; TYPE: PRT
; ORGANISM: unknown organism
; FEATURE:
; OTHER INFORMATION: unknown organism: amino acid sequence of neutrophilic
; OTHER INFORMATION: chemoattractant
; OTHER INFORMATION: released during direct alkaline hydrolysis of corneal proteins; t
; OTHER INFORMATION: polymorphonuclear leukocyte invasion into alkali-injured cornea
US-09-967-003-1

Query Match 52.0%; Score 13; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GP 2
DB 2 GP 3

RESULT 46
US-09-836-433-16
; Sequence 16, Application US/09836433
; Publication No. US20030049797A1
; GENERAL INFORMATION:
; APPLICANT: Yuki, Yoshikazu
; APPLICANT: Udaaka, Shigezo
; TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
; FILE REFERENCE: No. US20030049797A1 Assigned

; CURRENT APPLICATION NUMBER: US/09/836,433
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 3
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-836-433-16

Query Match 52.0%; Score 13; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
DB 1 GP 2

RESULT 47
US-09-755-630A-277
; Sequence 277, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASHWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTAINS
; FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
; CURRENT APPLICATION NUMBER: US/09/755,630A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 277
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-277

Query Match 52.0%; Score 13; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
DB 1 GP 2

RESULT 48
US-10-346-198-64
; Sequence 64, Application US/10346198
; Publication No. US20040043485A1
; GENERAL INFORMATION:
; APPLICANT: WESSLER, SUSAN R.
; APPLICANT: JIANG, NING
; APPLICANT: BAO, ZHIRONG
; APPLICANT: ZHANG, XIAOYU
; APPLICANT: EDDY, SEAN R.
; TITLE OF INVENTION: TRANSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
; FILE REFERENCE: 18465-0018
; CURRENT APPLICATION NUMBER: US/10/346,198
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/337,409
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 3

; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-346-198-64

Query Match 52.0%; Score 13; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
DB 2 GP 3

RESULT 49
US-10-363-208-192
; Sequence 192, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
US-10-363-208-192

Query Match 52.0%; Score 13; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
DB 1 GP 2

RESULT 50
US-10-232-838-3
; Sequence 3, Application US/10232838
; Publication No. US20030064053A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Shengjiang
; APPLICANT: Martini, Jean-Francois
; APPLICANT: Liu, Dayou
; TITLE OF INVENTION: MULTIVALENT PROTEIN CONJUGATE WITH MULTIPLE LIGAND-BINDING DOMAINS
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: 26050-707
; CURRENT APPLICATION NUMBER: US/10/232,838
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 06/316,718
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Linker sequence
US-10-232-838-3

Query Match 52.0%; Score 13; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
Db 1 GP 2

Search completed: September 7, 2004, 19:36:05
Job time : 123 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2004, 18:56:12 ; Search time 39 Seconds
(without alignments)
9.866 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	30	2 S74112	proline-rich antib
2	25	100.0	42	2 A34259	cytochrome P450mt4
3	25	100.0	49	1 NAXAB	anthopleurin B
4	25	100.0	57	2 I49627	testosterone 16a-h
5	25	100.0	58	2 I36690	cytochrome P450 2B
6	25	100.0	58	2 S16486	rRNA N-glycosidase
7	25	100.0	59	2 A36589	bactenecin 7 - bov
8	25	100.0	62	2 S19327	venom basic protei
9	25	100.0	64	2 S02055	Balbani ring prot
10	25	100.0	66	2 PNO644	hypothetical prote
11	25	100.0	70	2 A36650	protein F2401.6 [l
12	25	100.0	72	2 T22081	hypothetical prote
13	25	100.0	79	2 S01718	Balbani ring prot
14	25	100.0	84	2 J01356	Vi protein - Misca
15	25	100.0	87	2 P91363	hypothetical prote
16	25	100.0	90	2 T35074	hypothetical prote
17	25	100.0	90	2 A23515	hypothetical prote
18	25	100.0	91	2 AC3075	sarcosine oxidase
19	25	100.0	91	2 P98211	sarcosine oxidase
20	25	100.0	92	2 F72581	hypothetical prote
21	25	100.0	93	2 H96003	hypothetical prote
22	25	100.0	95	2 S01717	Balbani ring prot
23	25	100.0	97	2 S56134	hypothetical prote
24	25	100.0	101	2 S37068	NADH2 dehydrogenas
25	25	100.0	104	2 A41384	nicotinic acetylch
26	25	100.0	104	2 B41384	nicotinic acetylch
27	25	100.0	105	2 E72707	hypothetical prote
28	25	100.0	107	2 A44887	glucose transporte
29	25	100.0	109	2 T33239	synaptobrevin SNB-

30	25	100.0	109	2 F72666	hypothetical prote
31	25	100.0	111	2 S72737	adenine phosphorib
32	25	100.0	111	2 D72646	hypothetical prote
33	25	100.0	115	2 T34629	hypothetical prote
34	25	100.0	117	2 T21988	hypothetical prote
35	25	100.0	119	2 S69850	hypothetical prote
36	25	100.0	119	2 G72725	hypothetical prote
37	25	100.0	124	2 T03242	G-box binding fact
38	25	100.0	125	2 D72247	ribosomal protein
39	25	100.0	125	2 T03529	conserved hypotet
40	25	100.0	127	2 A49269	phospholipase A2 h
41	25	100.0	127	2 D75595	hypothetical prote
42	25	100.0	127	2 E87258	hypothetical prote
43	25	100.0	129	2 T36299	probable proline-r
44	25	100.0	131	2 T07973	hypothetical prote
45	25	100.0	132	2 A83293	conserved hypotet
46	25	100.0	133	2 T04081	probable ribosomal
47	25	100.0	134	2 A40959	secretin precursor
48	25	100.0	134	2 AG3080	conserved hypotet
49	25	100.0	134	2 B98206	hypothetical prote
50	25	100.0	134	2 T50607	hypothetical prote
51	25	100.0	135	2 S12549	hypothetical prote
52	25	100.0	137	2 T15609	hypothetical prote
53	25	100.0	140	2 G96603	unknown protein P1
54	25	100.0	143	2 A10838	probable membrane
55	25	100.0	144	1 JN0589	glucose-dependent
56	25	100.0	144	2 S71426	glucose-dependent
57	25	100.0	144	2 T03563	probable ribosomal
58	25	100.0	144	2 D83152	hypothetical prote
59	25	100.0	145	1 TNLJBT	trans-activating t
60	25	100.0	145	2 H75262	hypothetical prote
61	25	100.0	149	2 F73677	hypothetical prote
62	25	100.0	150	2 F76637	probable lipoprote
63	25	100.0	150	2 T46850	Asma protein (impo
64	25	100.0	151	2 A69195	transcription regu
65	25	100.0	153	2 AB2711	30S ribosomal prot

ALIGNMENTS

RESULT 1

S74112
proline-rich antibacterial protein - green crab (fragment)
C;Species: Carcinus maenas (green crab, common shore crab)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: S74112
R;Schnapp, D.; Kemp, G.D.; Smith, V.J.
Eur. J. Biochem. 240, 532-539, 1996
A;Title: Purification and characterization of a proline-rich antibacterial peptide, with
A;Reference number: S74112; MUID:97008941; PMID:8856051
A;Accession: S74112
A;Molecule type: protein
A;Residues: 1-30 <SCH>
A;Experimental source: haemocytes
C;Keywords: antibacterial

Query Match 100.0%; Score 25; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 85;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 15 GPRP 18

RESULT 2

A34259
cytochrome P450mt4, phenobarbital-inducible, mitochondrial, hepatic - rat (fragment)
N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Mar-1999
C;Accession: A34259

R;Shayiq, R.M.; Avadhani, N.G.
 Biochemistry 29, 866-873, 1990
 A;Title: A phenobarbital-inducible hepatic mitochondrial cytochrome P-450 immunochemical
 A;Reference number: A34259; MUID:90254127; PMID:2340279
 A;Accession: A34259
 A;Molecule type: protein
 A;Residues: 1-42 <SHA>
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: electron transfer; heme; liver; mitochondrion; monooxygenase; oxidoreductase

Query Match 100.0%; Score 25; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 33 GPRP 36

RESULT 3
 NAXAB
 Anthopleurin B - sea anemone (Anthopleura xanthogrammica)
 C;Species: Anthopleura xanthogrammica (Giant green sea anemone)
 C;Date: 31-Mar-1981 #sequence_revision 30-Jun-1987 #text_change 04-Oct-1996
 C;Accession: A92547; A94482; A01795
 R;Reimer, N.S.; Yasunobu, C.L.; Yasunobu, K.T.; Norton, T.R.
 J. Biol. Chem. 260, 8690-8693, 1985
 A;Title: Amino acid sequence of the Anthopleura xanthogrammica heart stimulant, anthopleurin B
 A;Reference number: A92547; MUID:85261226; PMID:4019448
 A;Accession: A92547
 A;Molecule type: protein
 A;Residues: 1-49 <REI>
 R;Bennett, C.D.
 unpublished results, cited by Norton, T.R., Fed. Proc. 40, 21-25, 1981

Query Match 100.0%; Score 25; DB 1; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 10 GPRP 13

RESULT 4
 I49627
 testosterone 16a-hydroxylase type c - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1999
 C;Accession: I49627
 R;Lakso, M.; Masaki, R.; Noshiro, M.; Negishi, M.
 Eur. J. Biochem. 195, 477-486, 1991
 A;Title: Structures and characterization of sex-specific mouse cytochrome P-450 genes as
 A;Reference number: I49625; MUID:91146586; PMID:1997326
 A;Accession: I49627
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-57 <RES>
 A;Cross-references: GB:M60359; NID:g192889; PIDN:AAA03650.1; PID:g192890
 C;Genetics:
 A;Gene: 16aoh-c
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; transmembrane protein

Query Match 100.0%; Score 25; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 33 GPRP 36

RESULT 5
 I53890
 cytochrome P450 2B15 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jun-1999
 C;Accession: I53890
 R;Nakayama, K.; Suwa, Y.; Mizukami, Y.; Sogawa, K.; Fujii-Kuriyama, Y.
 Gene 136, 333-336, 1993
 A;Title: Cloning and sequencing of a novel rat cytochrome P450 2B-encoding gene.
 A;Reference number: I53890; MUID:94124025; PMID:8294026
 A;Accession: I53890
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-58 <RES>
 A;Cross-references: GB:D17343; NID:9468474; PIDN:BAA04162.1; PID:9468475
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; transmembrane protein

Query Match 100.0%; Score 25; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 34 GPRP 37

RESULT 6
 S16486
 RNA N-glycosidase (EC 3.2.2.22) 5b - common soapwort (fragment)
 N;Alternate names: ribosome-inactivating protein SO-5b; saporin 5b
 C;Species: Saponaria officinalis (common soapwort)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 10-Oct-1997
 C;Accession: S16486
 R;Montecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Sorio, M.; Lappi, D.
 Int. J. Pept. Protein Res. 33, 263-267, 1989
 A;Title: N-terminal sequence of some ribosome-inactivating proteins.
 A;Reference number: S16331; MUID:89326691; PMID:27535596
 A;Accession: S16486
 A;Molecule type: protein
 A;Residues: 1-58 <MON>
 C;Superfamily: RNA N-glycosidase; rRNA N-glycosidase homology
 C;Keywords: glycosidase; hydrolase
 F;6-58/domain: rRNA N-glycosidase homology (fragment) <RNG>

Query Match 100.0%; Score 25; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 ||||
 Db 43 GPRP 46

RESULT 7
 A36589
 bacterenecin 7 - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-May-1997
 C;Accession: A36589
 R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
 J. Biol. Chem. 265, 18871-18874, 1990
 A;Title: Amino acid sequences of two proline-rich bacterenecins. Antimicrobial peptides of
 A;Reference number: A36589; MUID:91035404; PMID:2229048
 A;Accession: A36589

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-59 <FRA>
C;Superfamily: cathelin; cystatin homology

Query Match 100.0%; Score 25; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 24 GPRP 27

RESULT 8

S19327
venom basic proteinase inhibitor - leaf-nosed viper
N;Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C;Accession: S19327
R;Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991

A;Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
A;Reference number: S19327; MUID:92077130; PMID:1743283
A;Accession: S19327
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62 <SID>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 100.0%; Score 25; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 59 GPRP 62

RESULT 9

S02055
Balbiani ring protein 1-gamma (clone pC26) - midge (Chironomus pallidivittatus) (fragme
C;Species: Chironomus pallidivittatus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 17-Mar-2000
C;Accession: S02055
R;Lendahl, U.; Saiga, H.; Hoeoeg, C.; Edstroem, J.E.; Wieslander, L.
Genetics 117, 43-49, 1987

A;Title: Rapid and concerted evolution of repeat units in a Balbiani ring gene.
A;Reference number: S01717

A;Accession: S02055
A;Molecule type: mRNA
A;Residues: 1-64 <LEN>
A;Cross-references: EMBL:X08432
A;Note: the authors translated the codon AGA for residue 50 as Lys
C;Superfamily: unassigned Balbiani ring proteins

Query Match 100.0%; Score 25; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 6 GPRP 9

RESULT 10

FN0644
hypothetical protein 66 - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999

C;Accession: FN0644
R;Wray Jr., L.V.; Fisher, S.H.
Gene 130, 145-150, 1993
A;Title: The Streptomyces coelicolor ginR gene encodes a protein similar to other bacteri
A;Reference number: JN0831; MUID:93345814; PMID:7688332
A;Accession: FN0644
A;Molecule type: DNA
A;Residues: 1-66 <WRA>
A;Cross-references: GB:L03213
C;Genetics:
A;Start codon: GTG

Query Match 100.0%; Score 25; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 27 GPRP 30

RESULT 11

A96650
protein F2401.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: A96650
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.P.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <STO>
A;Cross-references: GB:AE005173; NID:G7940276; PIDN:AAF70835.1; GSPDB:GN00141
C;Genetics:
A;Gene: F2401.6
A;Map position: 1
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 100.0%; Score 25; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 62 GPRP 65

RESULT 12

T22081
hypothetical protein F41E7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T22081
R;Jennard, N.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19509
A;Accession: T22081
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-72 <WIL>
A;Cross-references: EMBL:Z68106; PIDN:CAA92131.1; GSPDB:GN000028; CESP:F41E7.8
A;Experimental source: clone F41E7
C;Genetics:

A;Gene: CESP:F41E7.8
A;Map position: X
A;Introns: 18/2

Query Match 100.0%; Score 25; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GRRP 4
|||
Db 41 GRRP 44

RESULT 13

S01718
Balbiani ring protein l-gamma (clone pCp28) - midge (*Chironomus pallidivittatus*) (fragment)

C;Species: *Chironomus pallidivittatus*
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 17-Mar-2000
C;Accession: S01718
R;Lendahl, U.; Saiga, H.; Hoeoeg, C.; Edstroem, J.E.; Wieslander, L.

Genetics 117, 43-49, 1987

A;Title: Rapid and concerted evolution of repeat units in a Balbiani ring gene.

A;Reference number: S01717

A;Accession: S01718

A;Molecule type: mRNA

A;Residues: 1-79 <LEN>

A;Cross-references: EMBL:X06434; NID:G2022; PID:G683548

A;Note: the authors translated the codon AGA for residue 30 as Lys

C;Superfamily: unassigned Balbiani ring proteins

Query Match 100.0%; Score 25; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GRRP 4
|||
Db 7 GRRP 10

RESULT 14

JQ1356

V1 protein - *Miscanthus streak virus*

C;Species: *Miscanthus streak virus*

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Oct-1999

C;Accession: JQ1356; JQ0919

R;Chatani, M.; Matsumoto, Y.; Mizuta, H.; Ikegami, M.; Boulton, M.I.; Davies, J.W.

J. Gen. Virol. 72, 2325-2331, 1991

A;Title: The nucleotide sequence and genome structure of the geminivirus *Miscanthus streak virus*

A;Reference number: JQ1355; MUID:92013947; PMID:1919519

A;Accession: JQ1356

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-84 <CHA>

A;Cross-references: DDBJ:D01030; NID:G222128; PID:BAA00837.1; PID:dl001301; PID:g222130

C;Comment: *Miscanthus streak virus* causes leaf streak.

Query Match 100.0%; Score 25; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GRRP 4
|||
Db 59 GRRP 62

RESULT 15

F87163

hypotheical protein [imported] - *Mycobacterium leprae*

C;Species: *Mycobacterium leprae*

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C;Accession: F87163

R;Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holt

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: F87163

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-87 <STO>

A;Cross-references: GB:AL450380; NID:gl3093653; PIDN:CAC30990.1; GSPDB:GN00147

C;Genetics:

A;Gene: ML2035

Query Match 100.0%; Score 25; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GRRP 4
|||
Db 24 GRRP 27

RESULT 16

T36074

hypotheical protein SCE126.04 - *Streptomyces coelicolor*

C;Species: *Streptomyces coelicolor*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T36074

R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1999

A;Reference number: Z21573

A;Accession: T36074

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-90 <OLI>

A;Cross-references: EMBL:AL049630; PIDN:CA840926.1; GSPDB:GN00070; SCOEDB:SCE126.04

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SCE126.04

Query Match 100.0%; Score 25; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GRRP 4
|||
Db 53 GRRP 66

RESULT 17

AC3515

hypotheical protein BMEII0045 [imported] - *Bruceella melitensis* (strain 16M)

C;Species: *Bruceella melitensis*

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C;Accession: AC3515

R;DeIvecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, I.

; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen *Bruceella melitensis*

A;Reference number: AD3252; PMID:11756688

A;Accession: AC3515

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-90 <KUR>

A;Cross-references: GB:AE008918; PIDN:AAL53286.1; PID:gl7984169; GSPDB:GN00191

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEII0045

A;Map position: II

Query Match 100.0%; Score 25; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GPRP 4
 ||||
 Db 84 GPRP 87

RESULT 18

AC3075
 sarcosine oxidase delta subunit [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AC3075
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan,
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm,
 sner, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; PMID:21608550; PMID:11743193
 A;Accession: AC3075
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-91 <KUR>
 A;Cross-references: GB:AE008689; PIDN:AAU45017.1; PID:g17742678; GSPDB:GN00187
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: soxD
 A;Map position: linear chromosome

Query Match 100.0%; Score 25; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 11 GPRP 14

RESULT 19

F98211
 sarcosine oxidase delta chain (sarcosine oxidase chain d) [imported] - Agrobacterium tum
 C;Species: Agrobacterium tumefaciens
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; PMID:11743194
 A;Accession: F98211
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-91 <KUR>
 A;Cross-references: GB:AE007870; PIDN:AAK89216.1; PID:g15159037; GSPDB:GN00170
 C;Genetics:
 A;Gene: AGR_L1276
 A;Map position: linear chromosome

Query Match 100.0%; Score 25; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 11 GPRP 14

RESULT 20

E72581
 hypothetical protein APES065 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C;Accession: E72581
 R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha,
 wa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru
 A;Reference number: A72450; PMID:99310339; PMID:10382966
 A;Accession: E72581
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-92 <KAW>
 A;Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80938.1; PID:d1044724; PID:g5105
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APES065

Query Match 100.0%; Score 25; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 57 GPRP 60

RESULT 21

H96003
 hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymb
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C;Accession: H96003
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
 A;Reference number: A9842; PMID:21396508; PMID:11481431
 A;Accession: H96003
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-93 <KUR>
 A;Cross-references: GB:AL591985; PIDN:CAC49696.1; PID:g15141183; GSPDB:GN00167
 A;Experimental source: strain 1021, megaplasmid pSymb
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heubal, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; PMID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMB21470
 A;Genome: plasmid

Query Match 100.0%; Score 25; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 88 GPRP 91

RESULT 22

S01717
 Balbiani ring protein 1-gamma (clone pCp20) - midge (Chironomus pallidivittatus) (fragment
 C;Species: Chironomus pallidivittatus
 C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 17-Mar-2000
 C;Accession: S01717
 R;Lerdahl, U.; Saiga, H.; Hoeoeg, C.; Edstroem, J.E.; Wieslander, L.
 Genetics 117, 43-49, 1987

A;Title: Rapid and concerted evolution of repeat units in a Balbiani ring gene.
 A;Reference number: S01717
 A;Accession: S01717

```

A:Molecule type: mRNA
A:Residues: 1-95 <LEN>
A:Cross-references: EMBL:X06431; NID:g7016; PID:g583545
A>Note: the authors translated the codon AGA for residue 42 as Lys
C:Superfamily: unassigned Balbiani ring proteins

Query Match      100.0%; Score 25; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 5 GPRP 8

RESULT 23
S56134
hypothetical protein - Thiosphaera pantotropha (fragment)
C:Species: Thiosphaera pantotropha
C>Date: 27-Oct-1995 #sequence_revision 26-Jul-1996 #text_change 08-Oct-1999
C:Accession: S56134; S50166
R:Birks, B.C.; Richardson, D.J.; Reilly, A.; Willis, A.C.; Ferguson, S.J.
Biochem. J. 309, 983-992, 1995
A:Title: The napSDABC gene cluster encoding the periplasmic nitrate reductase system of
A:Reference number: S56128; MUID:95366980; PMID:7639719
A:Accession: S56134
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-97 <BER>
A:Cross-references: EMBL:Z36773; NID:g600089; PIDN:CAA85349.1; PID:g6000956
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994

Query Match      100.0%; Score 25; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 48 GPRP 51

RESULT 24
S37068
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain K - Escherichia coli (strain AN387
N:Alternate names: complex 1 dehydrogenase, chain K; NADH dehydrogenase I, chain K; type
C:Species: Escherichia coli
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Jun-2002
C:Accession: S38320; S37068
R:Weidner, U.; Geier, S.; Ptocek, A.; Friedrich, T.; Leif, H.; Weiss, H.
J. Mol. Biol. 233, 109-122, 1993
A:Title: The gene locus of the proton-translocating NADH:ubiquinone oxidoreductase in Es
chondrial complex I.
A:Reference number: S38310; MUID:93389724; PMID:7690854
A:Accession: S38320
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <WEI>
A:Cross-references: EMBL:X68301; NID:g444012; PIDN:CAA48370.1; PID:g397908
A:Experimental source: strain AN387
C:Genetics:
A:Gene: nuck
A:Map position: 49.5 min
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C:Keywords: membrane-associated complex; NAD; oxidoreductase; transmembrane protein

Query Match      100.0%; Score 25; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 54 GPRP 57

RESULT 25
A41384
nicotinic acetylcholine receptor alpha chain - Chinese cobra (fragment)
C:Species: Naja naja atra (Chinese cobra)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: A41384
R:Neumann, D.; Barchan, D.; Horowitz, M.; Kochva, E.; Fuchs, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 7255-7259, 1989
A:Title: Snake acetylcholine receptor: Cloning of the domain containing the four extracel
A:Reference number: A41384; MUID:89386720; PMID:2780569
A:Accession: A41384
A:Molecule type: mRNA
A:Residues: 1-104 <NEU>
A:Cross-references: GB:M26388; NID:g213370; PIDN:AAA49384.1; PID:g213371
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match      100.0%; Score 25; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 44 GPRP 47

RESULT 26
B41384
nicotinic acetylcholine receptor alpha chain - checkered water snake (fragment)
C:Species: Natrix tessellata (checkered water snake)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: B41384
R:Neumann, D.; Barchan, D.; Horowitz, M.; Kochva, E.; Fuchs, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 7255-7259, 1989
A:Title: Snake acetylcholine receptor: cloning of the domain containing the four extracel
A:Reference number: A41384; MUID:89386720; PMID:2780569
A:Accession: B41384
A:Molecule type: mRNA
A:Residues: 1-104 <NEU>
A:Cross-references: GB:M26389; NID:g213378; PIDN:AAA49387.1; PID:g213379
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match      100.0%; Score 25; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 44 GPRP 47

RESULT 27
E72707
hypothetical protein APE1076 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E72707
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yanazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72707
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <KAW>
A:Cross-references: DDBJ:AF000060; NID:g5104188; PIDN:BAA80061.1; PID:d1043847; PID:g5104
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1076

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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000

C;Accession: F72666
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A;Reference number: A72450; PMID:10382966

A;Accession: F72666
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-109 <RAW>
A;Cross-references: DDBJ:AF000060; NID:G5104188; PIDN:BAA79734.1; PID:d10433520; PID:g5104
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0757
C;Superfamily: Aeropyrum pernix hypothetical protein APE0757

Query Match 100.0%; Score 25; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
Db 55 GPRP 58

RESULT 31
S72737
adenine phosphoriboxyltransferase homolog apt2 - Mycobacterium leprae
N;Alternate names: Bll177_C3_242 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72737
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid Bll177.
A;Reference number: S72694
A;Accession: S72737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <SMI>
A;Cross-references: EMBL:U00011; NID:g466907; PIDN:AAA17101.1; PID:g466826
C;Genetics:
A;Gene: apt2
A;Start codon: GTG
C;Superfamily: Mycobacterium leprae adenine phosphoriboxyltransferase homolog apt2

Query Match 100.0%; Score 25; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
Db 106 GPRP 109

RESULT 32
D72646
Hypothetical protein APE0602 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72646
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A;Reference number: A72450; PMID:99310339; PMID:10382966
A;Accession: D72646
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <RAW>
A;Cross-references: DDBJ:AP000060; NID:G5104188; PIDN:BAA79572.1; PID:d1043358; PID:g5104
A;Experimental source: strain K1


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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 45 GPRP 48

RESULT 38
D72247
ribosomal protein S13 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 12-Jun-2003
C:Accession: D72247
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: D72247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <ARN>
A:Cross-references: GB:AB001798; GB:AB000512; NID:94982033; PIDN:AAD36543.1; PID:9498204
C:Genetics:
A:Gene: TM1475
C:Superfamily: ribosomal protein S13/S18

Query Match 100.0%; Score 25; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 112 GPRP 115

RESULT 39
T03529
conserved hypothetical protein - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C:Accession: T03529
R:Vlcek, C.; Paces, V.; Malteev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A:Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A:Reference number: Z14955; MUID:97404404; PMID:9256491
A:Accession: T03529
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-125 <VLC>
A:Cross-references: EMBL:AF010496; NID:G3128256; PIDN:AAC16182.1; PID:G3128330
C:Genetics:
A:Map position: 1

Query Match 100.0%; Score 25; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 24 GPRP 27

RESULT 40
A49269
phospholipase A2 homolog otoconin-22 - African clawed frog
N:Alternate names: 22K aragonitic otoconial protein
C:Species: Xenopus laevis (African clawed frog)
C>Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C:Accession: A49269; A23737

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R;Pote, K.G.; Hauer III, C.R.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Kretsinger, R.H.
Biochemistry 32, 5017-5024, 1993
A:Title: Otoconin-22, the major protein of aragonitic frog otoconia, is a homolog of phos
A:Reference number: A49269; MUID:93264410; PMID:8494877
A:Accession: A49269
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-127 <POT>
A:Note: sequence extracted from NCBI backbone (NCBIP:132801)
R;Pote, K.G.
in NASA Space Biology, Halstead, T.W., ed., pp.205-209, NASA Office of Space Science and
A:Reference number: A23737
A:Accession: A23737
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19,'X',21-45,'X',47-50,'XNDQX',51-74,'Q',76-80,88-112,'X',114-115,'Y',117-1
C:Superfamily: phospholipase A2
F;26-120,28-44,43-99,49-127,50-92,59-85,78-90/Disulfide bonds: #status predicted

Query Match 100.0%; Score 25; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 122 GPRP 125

RESULT 41
D75595
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C:Accession: D75595
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; P
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036996; PMID:10567266
A:Accession: D75595
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <WHI>
A:Cross-references: GB:AE001862; GB:AE001825; NID:G6460468; PIDN:AAF12374.1; PID:G646066
C:Genetics:
A:Experimental source: strain R1
A:Gene: DRA0026
A:Map position: 2
C:Superfamily: Deinococcus radiodurans hypothetical protein DRA0026

Query Match 100.0%; Score 25; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 82 GPRP 85

RESULT 42
E87258
hypothetical protein CC0078 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87258
R;Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647

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A;Accession: E87258
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <STO>
A;Cross-references: GB:AE005673; NID:gl3421177; PIDN:AAK22065.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0078

Query Match      100.0%; Score 25; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
    ||||
Db 35 GPRP 38

RESULT 43
T36299
probable proline-rich protein - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Nov-2000
C;Accession: T36299
R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21603
A;Accession: T36299
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-129 <SEE>
A;Cross-references: EMBL:AL049919; PIDN:CAB42676.1; GSPDB:GN00070; SCOEDB:SCE7.17C
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE7.17C
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match      100.0%; Score 25; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
    ||||
Db 48 GPRP 51

RESULT 44
T07973
hypothetical protein, low CO2-inducible - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Jun-2000
C;Accession: T07973
R;Buraw, M.D.; Chen, Z.Y.; Sonanishi, A.; Moroney, J.V.
submitted to the EMBL Data Library, July 1998
A;Description: Identification of a novel cDNA induced under low CO2 conditions.
A;Reference number: Z16260
A;Accession: T07973
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-131 <BUR>
A;Cross-references: EMBL:AF081461; NID:G3420926; PIDN:AAK31958.1; PID:G3420927
A;Experimental source: strain WT 137
C;Superfamily: Chlamydomonas reinhardtii low CO2-inducible 14.2K protein

Query Match      100.0%; Score 25; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
    ||||
Db 73 GPRP 76

RESULT 45
A;Accession: PA2827
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <STO>
A;Cross-references: GB:AE004709; GB:AE004091; NID:G9948904; PIDN:AAK06215.1; GSPDB:GN0011
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2827
C;Superfamily: hypothetical protein YCL033C

Query Match      100.0%; Score 25; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
    ||||
Db 110 GPRP 113

RESULT 46
T04081
probable ribosomal protein S31 [imported] - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T04081
R;Nakamura, I.; Kaneya, N.; Aoki, T.; Tada, T.; Norita, E.; Kanzaki, H.; Uchimiya, H.
submitted to the EMBL Data Library, August 1994
A;Description: cDNA sequence of ribosomal protein S31 homolog from rice calli exposed to
A;Reference number: Z15193
A;Accession: T04081
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-133 <NAK>
A;Cross-references: EMBL:D38011; PIDN:BAA07208.1
A;Experimental source: subsp. Japonica, callus
C;Superfamily: rat ribosomal protein S26
C;Keywords: ribosome

Query Match      100.0%; Score 25; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
    ||||
Db 110 GPRP 113

RESULT 47
A40959
secretin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C;Accession: A40886; A40959; A35094; A32544
R;Ittoh, N.; Furuya, T.; Ozaki, K.; Ohta, M.; Kawasaki, T.
J. Biol. Chem. 266, 12595-12598, 1991
A;Title: The secretin precursor gene. Structure of the coding region and expression in tr
A;Reference number: A40886; MUID:91286291; PMID:2061329
A;Accession: A40886
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <ITO>
A;Cross-references: GB:M63984; NID:G206889; PIDN:AAA42127.1; PID:G206890

```

R;Kopin, A.S.; Wheeler, M.B.; Nishitani, J.; McBride, E.W.; Chang, T.; Chey, W.Y.; Leite Proc. Natl. Acad. Sci. U.S.A. 88, 5335-5339, 1991
 A>Title: The secretin gene: evolutionary history, alternative splicing, and development
 A;Reference number: A40959; MUID:91271384; PMID:1711228
 A;Accession: A40959
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-134 <KOP>
 A;Cross-references: GB:M4033; NID:g206891; PIDN:AAA42128.1; PID:g206892
 R;Kopin, A.S.; Wheeler, M.B.; Leiter, A.B.
 Proc. Natl. Acad. Sci. U.S.A. 87, 2293-2303, 1990
 A>Title: Secretin: structure of the precursor and tissue distribution of the mRNA.
 A;Reference number: A35094; MUID:90192795; PMID:2315322
 A;Accession: A35094
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-134 <KOP2>
 A;Cross-references: GB:M31495; NID:g206887; PIDN:AAA42126.1; PID:g206888
 R;Gossen, D.; Vandermeers, A.; Vandermeers-Piret, M.C.; Rathe, J.; Cauvin, A.; Robberech Biochem. Biophys. Res. Commun. 160, 862-867, 1989
 A>Title: Isolation and primary structure of rat secretin.
 A;Reference number: A32544; MUID:89246545; PMID:2719704
 A;Accession: A32544
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 33-59 <GOS>
 C;Superfamily: glucagon
 C;Keywords: duplication

Query Match 100.0%; Score 25; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 116 GPRP 119

RESULT 48

AG3080
 conserved hypothetical protein Atu4267 [imported] - Agrobacterium tumefaciens (strain C5
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AG3080
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AG3080
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-134 <KUR>
 A;Cross-references: GB:AB008689; PIDN:AAL45061.1; PID:g17742726; GSPDB:GN00187
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu4267
 A;Map position: linear chromosome

Query Match 100.0%; Score 25; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 102 GPRP 105

RESULT 49

B98206

hypothetical protein AGR_L1189 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
 C;Species: Agrobacterium tumefaciens
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C;Accession: B98206
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: B98206
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-134 <KUR>
 A;Cross-references: GB:AE007870; PIDN:AAK89172.1; PID:g15158986; GSPDB:GN00170
 C;Genetics:
 A;Gene: AGR_L1189
 A;Map position: linear chromosome

Query Match 100.0%; Score 25; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 102 GPRP 105

RESULT 50

T50607

hypothetical protein DKFZp434I1016.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C;Accession: T50607

R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Weil, B.; Wiemann, S.

submitted to the Protein Sequence Database, June 2000

A;Reference number: Z25141

A;Accession: T50607

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-134 <AAA>

A;Cross-references: EMBL:AL359560

A;Experimental source: adult testis; clone DKFZp434I1016

C;Genetics:

A;Note: DKFZp434I1016.1

Query Match 100.0%; Score 25; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 119 GPRP 122

Search completed: September 7, 2004, 19:02:10

Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2004, 18:45:46 ; Search time 23 Seconds
(without alignments)
9.056 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	9	1 FAR9_ASCSU	P43172 ascaris suu
2	25	100.0	30	1 AP65_CARMA	P82964 carcinus ma
3	25	100.0	49	1 TXAB_ANTXA	P01531 anthopleura
4	25	100.0	62	1 IVBT_ERIMA	P24541 eristocophi
5	25	100.0	72	1 VG18_BPMU	Q38625 bacterioph
6	25	100.0	74	1 YIAT_MYCTU	P19771 mycobacteri
7	25	100.0	97	1 YNAC_FAPRN	Q56353 paracoccus
8	25	100.0	98	1 PRRP_BOVIN	P81264 bos taurus
9	25	100.0	103	1 TAT_BIV06	P19564 bovine immu
10	25	100.0	104	1 ACHA_NAJNA	P14143 naja naja
11	25	100.0	109	1 V77_FPV70	P50785 human papil
12	25	100.0	114	1 KNL2_BOMMX	P83055 bombina max
13	25	100.0	117	1 RS26_CABEL	Q45499 caenorhabdi
14	25	100.0	120	1 GPR2_FIG	Q62786 sus scrofa
15	25	100.0	125	1 LG6C_HUMAN	Q95867 homo sapien
16	25	100.0	125	1 RS13_THENA	Q9X115 thermotoga
17	25	100.0	127	1 ACHA_NATTE	P14144 natrix tess
18	25	100.0	127	1 PA2H_XENLA	P41485 xenopus lae
19	25	100.0	132	1 MSRB_LEPIN	Q87748 leptospira
20	25	100.0	132	1 MSRB_PSEAE	Q51016 pseudomonas
21	25	100.0	133	1 RS26_ORYSA	P49216 oryza sativ
22	25	100.0	134	1 SECR_RAT	P13384 rattus norv
23	25	100.0	142	1 KGL1_HUMAN	Q9UJ90 homo sapien
24	25	100.0	144	1 GIP_MOUSE	P48756 mus musculu
25	25	100.0	144	1 GIP_RAT	Q06145 rattus norv
26	25	100.0	144	1 RS6_RHOCA	Q88126 rhodobacter
27	25	100.0	149	1 RS6_RHIME	Q92427 rhizobium m
28	25	100.0	151	1 MSRB_METTH	Q26807 methanobact
29	25	100.0	152	1 KNL1_BOMMX	Q90W88 bombina max
30	25	100.0	152	1 SDC6_HUMLT	P83684 humicola lu
31	25	100.0	153	1 RS6_AGR75	Q8U677 agrobacteri
32	25	100.0	153	1 SDC6_NEUCR	P07509 neurospora
33	25	100.0	153	1 SDC6_YEAST	P00445 saccharomyc

34	25	100.0	157	1 NUSB_XYLFA	Q9pes3 xylella fas
35	25	100.0	158	1 VG09_HSV11	Q00163 ictaluriid h
36	25	100.0	162	1 GTR4_CANFA	Q9xat2 canis famil
37	25	100.0	163	1 RR18_ORYSA	P12152 oryza sativ
38	25	100.0	165	1 NKG7_HUMAN	Q16617 homo sapien
39	25	100.0	170	1 FGFV_HUMAN	Q9hct0 homo sapien
40	25	100.0	175	1 PACA_CHICK	P41534 g glucagon-
41	25	100.0	190	1 BCT7_BOVIN	P19661 bos taurus
42	25	100.0	192	1 AP10_ARATH	Q92pw2 arabidopsis
43	25	100.0	194	1 RN74_MOUSE	Q9Zs2 mus musculu
44	25	100.0	196	1 KGUA_HUMAN	Q16774 homo sapien
45	25	100.0	197	1 KGUA_BOVIN	P46195 bos taurus
46	25	100.0	197	1 KGUA_MOUSE	Q64520 mus musculu
47	25	100.0	200	1 GD1S_BOVIN	Q9tu03 bos taurus
48	25	100.0	200	1 GD1S_MOUSE	Q61593 mus musculu
49	25	100.0	201	1 GD1S_HUMAN	P52566 homo sapien
50	25	100.0	201	1 YK86_MYCTU	Q10694 mycobacteri
51	25	100.0	205	1 FLRE_HUMAN	P30043 homo sapien
52	25	100.0	208	1 LED2_DEIRA	Q9r1i0 deinococcus
53	25	100.0	211	1 CP8D_MOUSE	Q8bz25 mus musculu
54	25	100.0	211	1 UREF_MYCTU	P50050 mycobacteri
55	25	100.0	215	1 CNO_MOUSE	Q8ved2 mus musculu
56	25	100.0	216	1 HAN2_CHICK	Q90690 gallus gall
57	25	100.0	217	1 HAN2_HUMAN	Q95300 homo sapien
58	25	100.0	217	1 HAN2_MOUSE	Q61039 m heart- an
59	25	100.0	219	1 TM21_MESAU	O35587 mesocricetu
60	25	100.0	225	1 ERF3_ARATH	O80339 arabidopsis
61	25	100.0	226	1 EXOV_RHIME	Q02731 rhizobium m
62	25	100.0	226	1 EXOV_RHIME	P14186 rhizobium s
63	25	100.0	228	1 MODB_RHOCA	Q08382 rhodobacter
64	25	100.0	228	1 TIG1_HUMAN	P49788 homo sapien
65	25	100.0	232	1 PYRP_PSEAE	Q59654 pseudomonas

ALIGNMENTS

RESULT 1

FAR9_ASCSU STANDARD; PRT; 9 AA.

ID FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF9.
OS Ascaris suum (Fig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -/- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;
AMIDATION.

Query Match 100.0%; Score 25; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

Db 3 GPRP 6

RESULT 2

AP65_CARMA

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ID AP65 CARMA STANDARD; PRT; 30 AA.
AC P2924;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Antibacterial 6.5 kDa protein (fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Hemocyte;
RX MEDLINE=97008941; PubMed=8856051;
RA Schnapp D., Kemp G.D., Smith V.J.;
RT "Purification and characterization of a proline-rich antibacterial
RT peptide, with sequence similarity to bactericin-7, from the haemocytes
RT of the shore crab, Carcinus maenas.";
RL Eur. J. Biochem. 240:532-539(1996).
CC -!- FUNCTION: Strong antimicrobial activity against P. imobilis and
CC M. luteus, less active against E. coli D22.
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW is: 6.5 kDa.
CC -!- SIMILARITY: TO BOVINE BACTENECIN 7.
DR PIR; S74112; S74112.
DR Antibiotic.
FT NON TER 30 30
SQ SEQUENCE 30 AA; 3305 MW; 6E2C2205934896C4 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 15 GPRP 18

RESULT 3
TXAB ANTXA STANDARD; PRT; 49 AA.
AC P01531;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Anthopleurin B (Toxin AP-B).
OS Anthopleura xanthogrammica (Giant green sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6112;
RN [1]
RP SEQUENCE.
RC TISSUE=Chidoblast;
RX MEDLINE=85261226; PubMed=4019448;
RA Reimer N.S., Yasunobu C.L., Yasunobu K.T., Norton T.R.;
RT "Amino acid sequence of the Anthopleura xanthogrammica heart
RT stimulant, anthopleurin-B.";
RL J. Biol. Chem. 260:8690-8693(1985).
RN [2]
RP SEQUENCE OF 1-28.
RX MEDLINE=81090973; PubMed=6109877;
RA Bennett C.D.;
RL Unpublished results, cited by:
RL Norton T.R.;
RL Fed. Proc. 40:21-25(1981).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=96027101; PubMed=7582896;
RA Monks S.A., Pallaghy P.K., Scanlon M.J., Norton R.S.;
RT "Solution structure of the cardiotonic polypeptide anthopleurin-B
RT and comparison with anthopleurin-A.";
RL Structure 3:791-803(1995).
CC -!- FUNCTION: Binds specifically to the sodium channel, thereby

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CC delaying its inactivation during signal transduction. Thus it
CC strongly stimulates mammalian cardiac muscle contraction.
CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
CC -!- MISCELLANEOUS: Anthopleurin B is the most potent peptide heart
CC stimulator isolated from the sea anemone.
CC -!- SIMILARITY: Belongs to the sea anemone sodium channel inhibitory
CC toxin family.
DR PIR; A92547; NAXAB.
DR PDB; IAPF; 11-JUL-96.
DR InterPro: IPR000693; Anemone_toxin.
DR Pfam; PF00706; toxin_4; 1.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
KW Cnidocyst; 3D-structure.
KW DISULFID 4 46
FT DISULFID 6 36
FT DISULFID 29 47
FT CONFLICT 12 13 RP -> PN (IN REF. 2).
FT CONFLICT 25 25 Y -> A (IN REF. 2).
FT STRAND 3 3
FT TURN 14 17
FT STRAND 21 23
FT TURN 26 27
FT TURN 31 32
FT TURN 38 39
FT STRAND 45 47
SQ SEQUENCE 49 AA; 5274 MW; 7BD237179065AE90 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 10 GPRP 13

RESULT 4
TXAB ERIMA STANDARD; PRT; 62 AA.
AC P24541;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Venom trypsin inhibitor.
OS Eristocophis macmahoni (Leaf-nosed viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Eristocophis.
OX NCBI_TaxID=8702;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=92077130; PubMed=1743283;
RA Siddiqui A.R., Zaidi Z.H., Josnwall H.;
RT "Purification and characterization of a Kunitz-type trypsin inhibitor
RT from leaf-nosed viper venom.";
RL FEBS Lett. 294:141-143(1991).
CC -!- FUNCTION: This protein inhibits trypsin and kallikrein.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S19327; S19327.
DR HSSP; P00981; 1DTK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 2 52 BY SIMILARITY.
FT DISULFID 11 35 BY SIMILARITY.
FT DISULFID 27 48 BY SIMILARITY.

```

FT ACT SITE 12 13 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 59 GPRP 62

RESULT 5
VGI8 BPWU
ID VGI8 BPWU STANDARD; PRT; 72 AA.
AC Q38625;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein gpi18 (E18 protein).
GN 18 OR E18.
OS Bacteriophage Mu.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC Mu-like viruses.
OC NCBI_TaxID=10677;
RN [1]
RP SEQUENCE FROM N.A.
RA Stoddard S.F., Howe M.M.;
RL Submitted (SEP-1987) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Priess H., Brauer B., Schmidt C., Kamp D.;
RT "Sequence of the left end of Mu."
EL (in) Symonds N., Toussaint A., van de Putte P., Howe M.M. (eds.);
RL Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press,
RL New York (1987).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=21920971; PubMed=11922669;
RX Morgan G.J., Hatfull G.F., Casjens S., Hendrix R.W.;
RT "Bacteriophage Mu genome sequence: analysis and comparison with
RT Mu-like phages in Haemophilus, Neisseria and Deinococcus."
RL J. Mol. Biol. 317:337-359(2002).
CC
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CC
CC EMBL; Y00419; CAA68476.1; -;
DR EMBL; M64097; AAA32410.1; -;
DR EMBL; AF083977; AAF01095.1; -;
KW Hypothetical protein.
SQ SEQUENCE 72 AA; 8444 MW; B29272F519B8E068 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 28 GPRP 31

RESULT 6
YIAL MYCTU
ID YIAL MYCTU STANDARD; PRT; 74 AA.
AC P19771;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

30-MAY-2000 (Rel. 39, Last annotation update)
DE Insertion element IS986 hypothetical 8.2 kDa protein (ORF1).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91141314; PubMed=1981088;
RA McAdam R.A., Hermans P.W.M., van Soelingen D., Zainuddin Z.F.,
RA Catty D., van Embden J.D.A., Dale J.W.;
RT "Characterization of a Mycobacterium tuberculosis insertion sequence
RT belonging to the IS3 family."
RL Mol. Microbiol. 4:1607-1613(1990).
CC -1- SIMILARITY: STRONG, TO M.TUBERCULOSIS INSERTION ELEMENT IS6110
CC HYPOTHETICAL 12.0 kDa PROTEIN.
CC
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CC
CC EMBL; X52471; CAA36708.1; -;
DR EMBL; X52471; CAA36708.1; -;
KW Hypothetical protein; Transposable element.
SQ SEQUENCE 74 AA; 8232 MW; 2700FA99DD4C9745 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 66 GPRP 69

RESULT 7
YNAC PARN
ID YNAC PARN STANDARD; PRT; 97 AA.
AC Q56353;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein in napC 3' region (Fragment).
OS Paracoccus pantotrophus (Thiosphaera pantotropha).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OC NCBI_TaxID=82367;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 35512 / LMD 82.5;
RX MEDLINE=95366980; PubMed=7639719;
RA Berks B.C., Richardson D.J., Reilly A., Willis A.C., Ferguson S.J.;
RT "The napEDABC gene cluster encoding the periplasmic nitrate reductase
RT system of Thiosphaera pantotropha."
RL Biochem. J. 309:983-992(1995).
CC
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CC
CC EMBL; Z36773; CAA85349.1; -;
DR EMBL; Z36773; CAA85349.1; -;
DR PIR; S56134; S56134.
KW Hypothetical protein.
FT NON TER 97
SQ SEQUENCE 97 AA; 10325 MW; B50B4E2C6BD38127 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
DB 48 GPRP 51

RESULT 8

PRRP_BOVIN STANDARD; PRT; 98 AA.
AC P81264;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prolactin-releasing peptide precursor (PRRP) (Prolactin-releasing
DE hormone) [Contains: Prolactin-releasing peptide PRR31; Prolactin-
DE releasing peptide PRR20].
GN PRH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN NCBI_TaxID=9913;
[1]

SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.

PC TISSUE=Brain;
RX MEDLINE=98268781; PubMed=9607765;
RA Kitama S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
RA Kurokawa T., Nishimura O., Cuda H., Fujino M.,
RT "A prolactin-releasing peptide in the brain."
RL Nature 393:272-276(1998).
CC -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the
CC expression of prolactin through its receptor GPR10. May stimulate
CC lactotrophs directly to secrete PRL.
CC -!- TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
CC
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CC

EMBL; AB015417; BAA29025.1; -;
KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.

FT SIGNAL 1 22
FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRR31.
FT PEPTIDE 33 53 PROLACTIN-RELEASING PEPTIDE PRR20.
FT PROPEP 58 98
FT MOD RES 53 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
SQ SEQUENCE 98 AA; 10544 MW; 08AC35A13B0FA908 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||||
DB 63 GPRP 66

RESULT 9

TAT_BIV06 STANDARD; PRT; 103 AA.
ID TAT_BIV06

AC P19564;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (S ORF).

GN TAT.
OS Bovine immunodeficiency virus (isolate 106) (BIV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11658;
[1]

SEQUENCE FROM N.A.

RX MEDLINE=90223985; PubMed=2183467;
RA Garvey K.J., Oberste M.S., Elser J.E., Braun M.J., Gonda M.A.;
RT "Nucleotide sequence and genome organization of biologically active
RT proviruses of the bovine immunodeficiency-like virus."
RL Virology 175:391-409(1990).
[2]

STRUCTURE BY NMR OF 68-81.

RX MEDLINE=96072972; PubMed=7502045;
RA Puglisi J.D., Chen L., Blanchard S., Frankel A.D.;
RT "Solution structure of a bovine immunodeficiency virus Tat-TAR
RT peptide-RNA complex."
RL Science 270:1200-1203(1995).

CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter.

CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).

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CC

EMBL; M32691; -; NOT_ANNOTATED_CDS.

DR PDB; 1BIV; 23-DEC-96.

DR PDB; 1MNB; 27-JAN-97.

DR HIV; M32691; SORFSBIV106.

DR InterPro; IPR001831; IV_Tat.

DR Pfam; PF00539; Tat; 1.

DR PRINTS; PR00055; HIVTARDOMAIN.

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;

KW 3D-structure.

SQ SEQUENCE 103 AA; 11739 MW; 28479ED907F06A55 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 103;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

|||||

DB 66 GPRP 69

RESULT 10

ACHA_NAJNA

ID ACHA_NAJNA STANDARD; PRT; 104 AA.

AC P14143;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha chain (Fragment).

OS Naja naja (Indian cobra).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Elapinae; Naja.

OX NCBI_TaxID=35670;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=89386720; PubMed=2780569;

RA Neumann D., Barchan D., Horowitz M., Kochva E., Fuchs S.;

RT "Snake acetylcholine receptor: cloning of the domain containing the

RT four extracellular cysteines of the alpha subunit."

RL Proc. Natl. Acad. Sci. U.S.A. 86:7255-7259(1989).

CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an

extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.

-1- SUBUNIT: Pentamer of two alpha chains, and one each of the beta, delta, and gamma chains.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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EMBL; M26388; AAA49384.1; -
 InterPro; IPR006202; Neur Chan LBD.
 InterPro; IPR006201; Neur Channel.
 Pfam; PF02931; Neur chan LBD; 1.
 PRINTS; PR00252; NR1ONCHANNEL.
 PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein.

FT NON_TER 1 1
 DOMAIN <1 >104 EXTRACELLULAR.
 FT DISULFID 10 24 BY SIMILARITY.
 FT DISULFID 74 75 ASSOCIATED WITH RECEPTOR ACTIVATION.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT NON_TER 104 104
 SQ SEQUENCE 104 AA; 12194 MW; 47A39E2C9BFA7A0 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 Db 44 GPRP 47

RESULT 11
 VE7_HPV70 STANDARD; PRT; 109 AA.
 AC P50785;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE E7 protein.
 GN E7.
 OS Human papillomavirus type 70.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=39457;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=8915087;
 RX MEDLINE=96249586; PubMed=8915087;
 RA Forslund O., Hansson B.G.;
 RT "Human papillomavirus type 70 genome cloned from overlapping PCR products: complete nucleotide sequence and genomic organization.";
 RL J. Clin. Microbiol. 34:738-744(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97060129; PubMed=8904450;
 RA Longuet M., Beaudenon S., Orth G.;
 RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70, related to the potentially oncogenic HPV39.";
 RL J. Clin. Microbiol. 34:738-744(1996).
 CC -1- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING ACTIVITIES.
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EMBL; U21941; AAC54851.1; -
 EMBL; U22461; AAC54881.1; -
 InterPro; IPR00148; Papi_E7.
 DR Pfam; PF00527; E7; 1.
 KW Early protein; Transcription regulation; Oncogene;
 KW DNA-binding; Trans-acting factor.
 FT SITE 66 69 C-XX-C MOTIF-1.
 FT SITE 101 104 C-XX-C MOTIF-2.
 SQ SEQUENCE 109 AA; 12657 MW; 2FD3C643DFAFT891 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
 Db 3 GPRP 6

RESULT 12
 KNL2_BOMX STANDARD; PRT; 114 AA.
 ID KNL2_BOMX
 AC P83055;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-FEB-2004 (Rel. 43, Last annotation update)
 DE Kininogen-2 precursor (BMK-2) [Contains: Maximakinin; Bradykinin; Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
 DE Maximakinin associated peptide].
 OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=161274;
 RN [1]
 RP SEQUENCE FROM N.A.; SEQUENCE OF 77-95 AND 105-114, AMIDATION, AND VARIANT LEU-74.
 RC TISSUE=Skin secretion, and Venom gland;
 RX MEDLINE=22830826; PubMed=12948837;
 RA Chen T., Bjourson A.J., McClean S., Orr D.F., O'Kane E.J., Rao P., Shaw C.;
 RA "Cloning of maximakinin precursor cDNAs from Chinese toad, Bombina maxima, venom.";
 RT Peptides 24:853-861(2003).
 RL Peptides 24:853-861(2003).
 CC -1- FUNCTION: Potent vasodilator. Binds B1 and B2 bradykinin receptors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the bradykinin family.

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EMBL; AJ440236; CAD29346.1; -
 DR Amphibian defense peptide; Vasodilator; Bradykinin; Repeat; Signal;
 KW Amidation; Pyrrolidone carboxylic acid; Polymorphism.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 114 KININOGEN-2.
 FT PEPTIDE 77 95 MAXIMAKININ.
 FT PEPTIDE 87 95 BRADYKININ.
 FT PEPTIDE 105 113 MAXIMAKININ POTENTIATING PEPTIDE.
 FT MOD_RES 105 105 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 113 113 AMIDATION (G-114 PROVIDE AMIDE GROUP).
 FT VARIANT 74 74 F -> L.
 SQ SEQUENCE 114 AA; 13361 MW; 51D4525AB970C853 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 85 GPRP 88

RESULT 13
 RS26_CABEL STANDARD; PRT; 117 AA.
 AC Q45499;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 40S ribosomal protein S26.
 GN RPS-26 OR F39B2.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RL Dobson R.;
 RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the S26E family of ribosomal proteins.
 CC -----
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 CC -----
 CC EMBL; Z92834; CAB07387.1; -;
 DR PIR; T21988; T21988.
 DR WormPep; F39B2.6; CE16012.
 DR InterPro; IPR000892; Ribosomal_S26E.
 DR Pfam; PF01283; Ribosomal_S26E; 1.
 DR PROSITE; PS00733; RIBOSOMAL_S26E; FALSE_NEG.
 KW Ribosomal protein.
 SQ SEQUENCE 117 AA; 13249 MW; 0FB79092B80B605D CRC64;

Query Match 100.0%; Score 25; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 114 GPRP 117

RESULT 14
 GTR2_PIG STANDARD; PRT; 120 AA.
 AC Q62786;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 2
 DE (Glucose transporter type 2, liver) (Fragment).
 GN SLC2A2 OR GLUT2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Canty J.N., Young R.F., Fallavollita J.A.;

Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: Facilitative glucose transporter. This isoform likely
 mediates the bidirectional transfer of glucose across the plasma
 membrane of hepatocytes and is responsible for uptake of glucose
 by the beta cells; may comprise part of the glucose-sensing
 mechanism of the beta cell. May also participate with the
 Na(+)/glucose cotransporter in the transcellular transport of
 glucose in the small intestine and kidney (By similarity).
 -1- SUBCELLULAR LOCATION: Integral membrane protein.
 -1- SIMILARITY: Belongs to the sugar transporter family. Glucose
 transporter subfamily.
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 CC -----
 CC EMBL; AF054835; AAC12737.1; -;
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub_transporter.
 DR InterPro; IPR005829; Sug_transporter.
 DR InterPro; IPR003663; Sugar_transp.
 DR Pfam; PF00083; sugar_tr; 1.
 DR PRINTS; PR00171; SUGTRNSPOT.
 DR PROSITE; PS00850; MFS; 1.
 DR PROSITE; PS00215; SUGAR_TRANSPORT_1; PARTIAL.
 DR PROSITE; PS00211; SUGAR_TRANSPORT_2; PARTIAL.
 KW Transmembrane; Sugar transporter; Transport; Multigene family.
 FT NON TER 1 1
 FT TRANSMEM 2 22 9 (POTENTIAL).
 FT DOMAIN 23 26 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 27 47 10 (POTENTIAL).
 FT DOMAIN 48 56 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 57 77 11 (POTENTIAL).
 FT DOMAIN 78 84 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 85 105 12 (POTENTIAL).
 FT DOMAIN 106 120 CYTOPLASMIC (POTENTIAL).
 FT NON TER 120 120
 SQ SEQUENCE 120 AA; 13503 MW; D5F73168DBF03203 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 DB 53 GPRP 56

RESULT 15
 LG6C_HUMAN STANDARD; PRT; 125 AA.
 AC O95867;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lymphocyte antigen 6 complex locus G6C protein precursor (Protein
 DE NG24).
 GN LV6G6C OR NG24 OR C6ORF24.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22074936; PubMed=12079290;
 RA Mallya M., Campbell R.D., Aguado B.;
 RT "Transcriptional analysis of a novel cluster of LY-6 family members in
 RT the human and mouse major histocompatibility complex: five genes with
 RT many splice forms.";

Genomics 80:113-123 (2002).

[2]

SEQUENCE FROM N.A.

Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

Abdasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

Lasky S., Hood L.,

Sequence of the human major histocompatibility complex class III

region."

Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE FROM N.A.

Shina S., Tamiya G., Oka A., Inoko H.,

"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."

Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

-1- SUBCELLULAR LOCATION: Secreted (Potential).

-1- SIMILARITY: SOME, TO LY-6/UPAR DOMAIN.

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EMBL: AJ315533; CAC85539.1; -

EMBL: AF129756; AAD18076.1; -

EMBL: AP000504; BAB63379.1; -

Genew: HGNC:13936; LY6G6C.

Signal.

1 18 POTENTIAL.

19 125 LYMPHOCYTE ANTIGEN 6 COMPLEX LOCUS G6C

FT CHAIN

FT SIGNAL

FT CHAIN

SEQUENCE 125 AA; 13821 MW; 9ED7549894C71311 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 125;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

Db 101 GPRP 104

RESULT 16

RS13 THEME

ID RS13 THEME STANDARD; PRT; 125 AA.

AC Q9X1I5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE 30S ribosomal protein S13.

GN RPSM OR TM1475.

OS Thermotoga maritima.

OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

OX NCBI_TaxID=2336;

RN [1]_TaxID=2336;

SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;

RX MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Vasek J.A., Linher K.D., Garrett M.M.,

Steward A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima."

RL Nature 399:323-329 (1999).

-1- FUNCTION: Located at the top of the head of the 30S subunit, it

contacts several helices of the 16S rRNA. In the 70S ribosome it

contacts the 23S rRNA (bridge B1a) and protein L5 of the 50S

subunit (bridge B1b), connecting the 2 subunits; these bridges are

implicated in subunit movement. Contacts the tRNAs in the A and P-

sites (By similarity).

-1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a loose

heterodimer with protein S19. Forms two bridges to the 50S subunit

in the 70S ribosome (By similarity).

-1- SIMILARITY: Belongs to the S13p family of ribosomal proteins.

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EMBL: AB001798; AAD36543.1; -

PIR: D72247; D72247.

TIGR: TM1475; -

HAMAP: MF_01315; -; 1.

InterPro: IPR001892; Ribosomal_S13.

Pfam: PF00416; Ribosomal_S13; 1.

ProDom: PD001363; Ribosomal_S13; 1.

PROSITE: PS00646; RIBOSOMAL_S13_1; 1.

PROSITE: PS00159; RIBOSOMAL_S13_2; 1.

Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding;

Complete proteome.

SEQUENCE 125 AA; 14432 MW; 55E66DF6FA15097 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 125;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

Db 112 GPRP 115

RESULT 17

ACHA NATTE

ID ACHA NATTE STANDARD; PRT; 127 AA.

AC P14144;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha chain (Fragment).

OS Matrix tessellata (Dice snake) (Checked water snake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Colubridae; Natricinae; Matrix.

OX NCBI_TaxID=8584;

RN [1]

SEQUENCE FROM N.A.

RP TISSUE=Liver;

RX MEDLINE=89386720; PubMed=2780569;

RA Neumann D., Barchan D., Horowitz M., Kochva E., Fuchs S.;

"Snake acetylcholine receptor: cloning of the domain containing the

four extracellular cysteines of the alpha subunit."

Proc. Natl. Acad. Sci. U.S.A. 86:7255-7259 (1989).

-1- FUNCTION: After binding acetylcholine, the AChR responds by an

extensive change in conformation that affects all subunits and

leads to opening of an ion-conducting channel across the plasma

membrane. Does not bind alpha-bungarotoxin.

-1- SUBUNIT: Pentamer of two alpha chains, and one each of the beta,

delta, and gamma chains.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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CC ENBL; M26389; AAA49387.1; -
 CC ENBL; M30045; AAA60451.1; -
 CC PIR; B41384; B41384
 CC InterPro; IPR006202; Neur_chan_LBD.
 CC InterPro; IPR006201; Neur_chan_LBD.
 CC Pfam; PF02931; Neur_chan_LBD; 1.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein.
 CC NON_TER 1 127
 CC DOMAIN 1 127
 CC DISULFID 33 47
 CC DISULFID 97 98
 CC SITE 92 92
 CC SITE 94 94
 CC SITE 99 99
 CC SITE 99 99
 CC CARBOHYD 46 46
 CC CARBOHYD 94 94
 CC CONFLICT 39 39
 CC CONFLICT 54 54
 CC CONFLICT 59 59
 CC CONFLICT 62 62
 CC CONFLICT 64 64
 CC NON_TER 127 127
 CC SEQUENCE 127 AA; 14740 MW; 66740A006B6B2D7 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 127;

Best Local Similarity 100.0%; Pred. No. 1.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

DB 67 GPRP 70

RESULT 18

PA2H_XENLA

ID PA2H_XENLA STANDARD; PRT; 127 AA.

AC P41485;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Phospholipase A2 homolog otoconin-22 (Oc22).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE.

RX MEDLINE=93264410; PubMed=8494877;

RA Pote K.G., Hauer C.R. III, Michel H., Shabanowitz J., Hunt D.F.,

RA Kretzinger R.H.;

RT "Otoconin-22, the major protein of aragonitic frog otoconia, is a

RT homolog of phospholipase A2.";

RL Biochemistry 32:5017-5024(1993).

CC -! FUNCTION: Major protein of the aragonitic otoconia. It is unlikely

CC that this protein has phospholipase A2 activity.

CC -! SUBUNIT: Monomer (Probable).

CC -! SUBCELLULAR LOCATION: Secreted (By similarity).

CC -! TISSUE SPECIFICITY: Otoconial membrane in the maculae of the

CC sacculle and utricle. Otoconia are composites of proteins and

CC inorganic crystals formed in the peripheral portion of the

CC vestibular system of vertebrates. The otoconial membranes contain

CC small crystals of calcium carbonate known as otoliths (ear stones)

CC if there is a single deposit or as otoconia (ear dust) if there

CC are many. Each mineral polymorph of otoconia has a protein unique

CC to that polymorph.

CC -! SIMILARITY: Belongs to the phospholipase A2 family.

CC PIR; A49269; A49269.

CC HSSP; P00593; 4BP2.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD00303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1

DR PROSITE; PS00118; PA2_HIS; FALSE_NEG.

DR PROSITE; PS00119; PA2_ASP; 1.

KW Glycoprotein.

FT DISULFID 26 120

FT DISULFID 28 44

FT DISULFID 43 99

FT DISULFID 49 127

FT DISULFID 50 92

FT DISULFID 59 85

FT DISULFID 78 90

FT CARBOHYD 20 20

FT CARBOHYD 113 113

SQ SEQUENCE 127 AA; 14630 MW; 996A448766859BCE CRC64;

Query Match 100.0%; Score 25; DB 1; Length 127;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

DB 122 GPRP 125

RESULT 19

MSRB_LEPIN

ID MSRB_LEPIN STANDARD; PRT; 132 AA.

AC Q87M8;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6).

GN MSRB OR LA0824.

OS Leptospira interrogans.

OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.

OX NCBI_TaxID=173;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

RX MEDLINE=22598143; PubMed=12712204;

RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

RA Zhang Y.-X., Xiong H., Lu L.-P., Jiang H.-Q., Jia J., Tu Y.-F.,

RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

RA Xu J.-G., Zhao G.-P.;

RT "Unique physiological and pathogenic features of Leptospira

RT interrogans revealed by whole-genome sequencing.";

RL Nature 422:888-893(2003).

CC -! Protein L-methionine S-oxide + reduced thioredoxin =

CC -! SIMILARITY: Belongs to the msrB Met sulfoxide reductase family.

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CC -----

CC EMBL; AE011268; AAN48023.1; ALT_INIT.

DR HAMAP; MF_01400; -1

DR InterPro; IPR002579; DUF25.

DR Pfam; PF01641; SelR; 1.

DR ProDom; PD004057; DUF25; 1.

DR TIGRFAMs; TIGR00357; TIGR00357; 1.

KW Oxidoreductase; Complete proteome.

```
PT ACT SITE 121 121 BY SIMILARITY.
SQ SEQUENCE 132 AA; 14848 MW; 3B9DA6715CDF55E5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 132;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 112 GPRP 115

RESULT 20
MSRB_PSEAE
ID _MSRB_PSEAE STANDARD; PRT; 132 AA.
AC Q91016;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Peptide methionine sulfoxide reductase msrb (EC 1.8.4.6).
GN MSRB OR PA2827
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huihnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy R., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin =
CC protein L-methionine S-oxide + reduced thioredoxin.
CC -1- SIMILARITY: Belongs to the marB Met sulfoxide reductase family.
CC
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CC
CC -----
CC EMBL; D38011; BAA07208.1; -
CC FIR; T04081; T04081.
CC Gramene; P49216; -
CC InterPro; IPR000892; Ribosomal_S26E.
CC Pfam; PF01283; Ribosomal_S26e; 1.
CC PROSITE; PS00733; RIBOSOMAL_S26E; 1.
CC Ribosomal protein.
CC SEQUENCE 133 AA; 15016 MW; 8455305124690178 CRC64;
SQ
Query Match 100.0%; Score 25; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 110 GPRP 113

RESULT 22
SECR_RAT
ID _SECR_RAT STANDARD; PRT; 134 AA.
AC P11384;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Secreitin precursor.
GN SCT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90192795; PubMed=2315322;
RA Kopin A.S., Wheeler M.B., Leiter A.B.;
RT "Secreitin: structure of the precursor and tissue distribution of the
RT mRNA."
RN Proc. Natl. Acad. Sci. U.S.A. 87:2299-2303(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91271384; PubMed=1711128;
RA Kopin A.S., Wheeler M.B., Nishitani J., McBride E.W., Chang T.M.,
RA Chey W.Y., Leiter A.B.;
RT "The secretin gene: evolutionary history, alternative splicing, and
RT developmental regulation."
RN Proc. Natl. Acad. Sci. U.S.A. 88:5335-5339(1991).
RL
```

[3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=91286291; PubMed=2061329;
 RX Itoh N., Furuya T., Ozaki K., Kawasaki T.;
 RA "The secretin precursor gene. Structure of the coding region and
 RT expression in the brain".
 RL J. Biol. Chem. 266:12595-12598(1991).
 RN SEQUENCE OF 33-59.
 RX MEDLINE=89246545; PubMed=2719704;
 RC Gossen D., Vandermeers A., Vandermeers-Piret M.-C., Rathe J.,
 RA Cauvin A., Robberecht P., Christophe J.;
 RT "Isolation and primary structure of rat secretin";
 RL Biochem. Biophys. Res. Commun. 160:862-867(1989).
 CC -!- FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice
 CC and secretion of NaHCO(3)-rich bile and inhibits HCl production by
 CC the stomach.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the glucagon family.
 CC
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 CC
 CC ENBL; M31495; AAA42126.1; -;
 DR ENBL; M64033; AAA42128.1; -;
 DR ENBL; M63984; AAA42127.1; -;
 DR PIR; A40886; A40959.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 DR Glucagon family; Hormone; Amidation;
 KW Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PEPTIDE 33 59 SECRETIN.
 FT MOD_RES 59 59 AMIDATION (G-60 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 134 AA; 15072 MW; D9FA1A4C1F7C6E6 CRC64;
 Query Match 100.0%; Score 25; DB 1; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GRRP 4
 DB 116 GRRP 119
 RESULT 23
 KCIL_HUMAN STANDARD; PRT; 142 AA.
 ID KCIL_HUMAN
 AC Q9UJ90;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Potassium voltage-gated channel subfamily E member 1-like protein
 DE (AMME syndrome candidate gene 2 protein) (AMMECR2 protein).
 GN KCNE1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neuron, and Placenta;
 RX MEDLINE=99425286; PubMed=10493825;
 RA Piccini M., Vitelli F., Seri M., Galletta L.J.V., Moran O.,
 RA Bulfone A., Banfi S., Pober B., Renieri A.

RT "KCNE1-like gene is deleted in AMME contiguous gene syndrome:
 RT Identification and characterization of the human and mouse homologs.";
 RL Genomics 60:251-257(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart, skeletal muscle,
 CC brain, spinal cord and placenta.
 CC -!- DISEASE: Defects in KCNE1 may be a cause of AMME complex
 CC (MIM:300194); also known as Alport syndrome, mental retardation,
 CC midface hypoplasia and elliptocytosis, and of additional mild
 CC abnormalities of the heart. The AMME complex is a contiguous gene
 CC deletion syndrome.
 CC -!- SIMILARITY: Belongs to the potassium channel KCNE family.
 CC
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 CC
 CC ENBL; AJ012743; CAB58359.1; -;
 DR ENBL; BC035330; AAH35330.1; -;
 DR Genew; HGNC:6241; KCNE1.
 DR MIM; 300328; -;
 DR MIM; 300194; -;
 DR GO; GO:0008076; C: voltage-gated potassium channel complex; TAS.
 DR GO; GO:0008016; P: regulation of heart rate; TAS.
 DR Transmembrane; Glycoprotein; Alport syndrome; Deafness;
 KW Elliptocytosis.
 KW TRANSMEM 61 81 POTENTIAL.
 FT DOMAIN 82 142 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 25 25 N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD 25 25 N-LINKED (GLCNAC...); (POTENTIAL).
 SQ SEQUENCE 142 AA; 14993 MW; ED8EC611CDE66BFE CRC64;
 Query Match 100.0%; Score 25; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GRRP 4
 DB 32 GRRP 35
 RESULT 24
 GIP_MOUSE STANDARD; PRT; 144 AA.
 ID GIP_MOUSE
 AC P48756;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Gastric inhibitory polypeptide precursor (GIP) (Glucose-dependent
 GN insulinotropic polypeptide)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96350462; PubMed=8764827;
 RA Schieldrop P.J., Gelling R.W., Elliot R., Hewitt J., Kieffer T.J.,
 RA McIntosh C.H.S., Pederson R.A.;
 RT "Isolation of a murine glucose-dependent insulinotropic polypeptide
 RT (GIP) cDNA from a tumor cell line (STC-14) and quantification of
 RT glucose-induced increases in GIP mRNA";
 RL Biochim. Biophys. Acta 1308:111-113(1996).
 CC -!- FUNCTION: Potent stimulator of insulin secretion and relatively
 CC poor inhibitor of gastric acid secretion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the glucagon family.
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 CC -----
 DR EMBL; U34295; AAC52731.1; -;
 DR PIR; S71426; S71426.
 DR HSP; P01274; 1GCG.
 DR MGP; MGI107504; GIP.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 DR Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PROPEP 22 42
 FT PEPTIDE 44 85 GASTRIC INHIBITORY POLYPEPTIDE.
 FT PROPEP 87 144
 SQ SEQUENCE 144 AA; 16359 MW; 26E718665D4DA8C3 CRC64;
 Query Match 100.0%; Score 25; DB 1; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db |||||
 36 GPRP 39
 RESULT 25
 ID_GIP_RAT STANDARD; PRT; 144 AA.
 AC Q06145;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Gastric inhibitory polypeptide precursor (GIP) (Glucose-dependent
 DE insulinotropic polypeptide).
 GN GIP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Duoenum;

RX MEDLINE=93119451; PubMed=1476614;
 RA Sharma S.K., Austin C., Howard A., Lo G., Nicholl C.G., Lagon S.;
 RT "Characterization of rat gastric inhibitory peptide cDNA";
 RL J. Mol. Endocrinol. 9:265-272(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Jejunum;
 RX MEDLINE=93189623; PubMed=8446620;
 RA Tseng C.C., Jabcoe L.A., Landau S.B., Williams S.K., Wolfe M.;
 RT "Glucose-dependent insulinotropic peptide: structure of the precursor
 RT and tissue-specific expression in rat";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1992-1996(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Intestine;
 RX MEDLINE=92379094; PubMed=1380834;
 RA Higashimoto Y., Liddle R.A., Simchok J.;
 RT "Molecular cloning of rat glucose-dependent insulinotropic peptide
 RT (GIP)";
 RL Biochim. Biophys. Acta 1132:72-74(1992).
 CC -!- FUNCTION: Potent stimulator of insulin secretion and relatively
 CC poor inhibitor of gastric acid secretion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the glucagon family.
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 CC -----
 DR EMBL; X66724; CAA47256.1; -;
 DR EMBL; Z19564; CAA79621.1; -;
 DR EMBL; L88831; AAA41225.1; -;
 DR EMBL; M92916; AAA41237.1; -;
 DR PIR; JN0589; JN0589.
 DR HSP; P01274; 1GCG.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 DR Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PROPEP 22 42
 FT PEPTIDE 44 85 GASTRIC INHIBITORY POLYPEPTIDE.
 FT PROPEP 87 144
 SQ SEQUENCE 144 AA; 16401 MW; 091D7617459C6032 CRC64;
 Query Match 100.0%; Score 25; DB 1; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db |||||
 36 GPRP 39
 RESULT 26
 ID_RHOCA STANDARD; PRT; 144 AA.
 AC C88126;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S6.
 GN RPS6.
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1061;

RN SEQUENCE FROM N.A.
RC STRAIN=SB1003 / St Louis;
RX MEDLINE=97404404; PubMed=9256491;
RA Vilek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.,
RT "Sequence of a 189-kb segment of the chromosome of Rhodospirillum rubrum
capsulatus SB1003";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
CC -!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
similarity).
CC -!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
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CC
CC EMBL; AF010496; AAC16216.1; -.
DR PIR; T03563; T03563.
DR HAMAP; MF 00360; -; 1.
DR InterPro; IPR000529; Ribosomal_S6.
DR Pfam; PF01250; Ribosomal_S6; 1.
DR ProDom; PD003809; Ribosomal_S6; 1.
DR TIGRFAMs; TIGR00166; S6; 1.
DR PROSITE; PS01048; RIBOSOMAL_S6; FALSE_NEG.
KW Ribosomal protein; rRNA-binding.
SQ SEQUENCE 144 AA; 16363 MW; 39A45DF2617143AD CRC64;

Query Match 100.0%; Score 25; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 GPRP 4
DB 138 GPRP 141

RESULT 27
RS6_RHIME STANDARD; PRT; 149 AA.
ID RS6_RHIME STANDARD; PRT; 149 AA.
AC Q2QZ7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S6
GN RPSF OR K01138 OR SMC00568.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=2136507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gilbert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
similarity).
CC -!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
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CC
CC EMBL; AL591786; CAC45717.1; -.
DR HAMAP; MF 00360; -; 1.
DR InterPro; IPR000529; Ribosomal_S6.
DR Pfam; PF01250; Ribosomal_S6; 1.
DR ProDom; PD003809; Ribosomal_S6; 1.
DR TIGRFAMs; TIGR00166; S6; 1.
DR PROSITE; PS01048; RIBOSOMAL_S6; FALSE_NEG.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 149 AA; 17274 MW; 15766B6EAE7F18C CRC64;

Query Match 100.0%; Score 25; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 GPRP 4
DB 129 GPRP 132

RESULT 28
MSRB_METH STANDARD; PRT; 151 AA.
ID MSRB_METH STANDARD; PRT; 151 AA.
AC Q26807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6).
GN MSRB OR MTH711.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics";
RL J. Bacteriol. 179:7135-7155(1997).
CC -!- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thiorodoxin =
protein L-methionine S-oxide + reduced thiorodoxin.
CC -!- SIMILARITY: Belongs to the msrB Met sulfoxide reductase family.
CC
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CC
CC EMBL; AE000850; AAB85216.1; -.
DR PIR; A69195; A69195.
DR HAMAP; MF 01400; -; 1.
DR InterPro; IPR002579; DUF25.
DR Pfam; PF01641; SelR; 1.
DR ProDom; PD004057; DUF25; 1.
DR TIGRFAMs; TIGR00357; TIGR00357; 1.
KW Oxidoreductase; Complete proteome.
FT ACI_SITE 136 BY SIMILARITY
SQ SEQUENCE 151 AA; 17302 MW; 6D11C52CEB186033 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
127 GPRP 130

Db

RESULT 29
KX11_BOMMX
ID KX11_BOMMX STANDARD; PRT; 152 AA.
AC Q90W88;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Kininogen-1 precursor (BMK-1) [Contains: Maximakinin; Bradykinin].
OS Bombina maxima (giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF MAXIMAKININ, AND SYNTHESIS OF
RP MAXIMAKININ.
RC TISSUE=Skin secretion, and Venom gland;
RX MEDLINE=22830826; PubMed=12948837;
RA Chen T., Bjournson A.J., McClean S., Orr D.F., O'Kane E.J., Rao P.,
RA Shaw C.;
RT "Cloning of maximakinin precursor cDNAs from Chinese toad, Bombina
RL maxima, venom.";
RL Peptides 24:853-861(2003).
CC -!- FUNCTION: Potent vasodilator. Binds B1 and B2 bradykinin
CC receptors.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bradykinin family.
CC
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CC
CC
CC EMBL; AJ315488; CAC48026.2;
KW Amphibian defense peptide; Vasodilator; Bradykinin; Repeat; Signal.
FT SIGNAL 1 23
FT CHAIN 24 152
FT PEPTIDE 41 59 KININOGEN-1.
FT PEPTIDE 51 59 MAXIMAKININ.
FT PEPTIDE 69 87 BRADYKININ.
FT PEPTIDE 79 87 MAXIMAKININ.
FT PEPTIDE 97 115 BRADYKININ.
FT PEPTIDE 107 115 MAXIMAKININ.
FT PEPTIDE 125 143 MAXIMAKININ.
FT PEPTIDE 135 143 MAXIMAKININ.
SQ SEQUENCE 152 AA; 17604 MW; B59B31389D837686 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
49 GPRP 52

Db

RESULT 30
SODC_HUMLT
ID SODC_HUMLT STANDARD; PRT; 152 AA.
AC P83684;
DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
OS Humicola lutea.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=253246;
RN [1]
RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, MASS SPECTROMETRY,
RP AND GLYCOSYLATION.
RC STRAIN=103;
RA Dolashka-Angelova P., Stevanovic S., Dolashki A., Angelova M.,
RA Serkedjieva J., Pashova S., Zacharieva S., Voelter W.,
RT "Structural and functional analyses of glycosylated Cu/Zn-superoxide
RT dismutase from the fungal strain Humicola lutea 103, cultivated in
RT copper stress.";
RT J. Biol. Chem. 278:0-0(2003).
RN [2]
RP SEQUENCE OF 1-35, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBUNIT, AND
RP MASS SPECTROMETRY.
RC STRAIN=103; TISSUE=Mycelium;
RX MEDLINE=2128675; PubMed=11390695;
RA Angelova M., Dolashka-Angelova P., Ivanova E., Serkedjieva J.,
RA Sloskova L., Pashova S., Toshkova R., Vassilev S., Simeonov I.,
RA Hartmann H.-J., Stoeva S., Weser U., Voelter W.,
RT "A novel glycosylated Cu/Zn-containing superoxide dismutase:
RT production and potential therapeutic effect.";
RL Microbiology 147:1641-1650(2001).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) +
CC H(2)O(2).
CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MASS SPECTROMETRY: MW=15935; METHOD=MALDI.
CC -!- MASS SPECTROMETRY: MW=15844.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
DR InterPro: IPR001424; SOD_CU_ZN.
DR Pfam: PF00080; sdcu; 1_CU_ZN.
DR PRINTS; PR00068; CUZNDISWTASE.
DR ProDom; PD000469; SOD_CU_ZN; 1.
DR PROSITE; PS00087; SOD_CU_ZN; 1.
DR PROSITE; PS00332; SOD_CU_ZN; 1.
KW Antioxidant; Oxidoreductase; Metal-binding;
KW Copper; Zinc; Glycoprotein.
FT METAL 46 46 COPPER (BY SIMILARITY).
FT METAL 48 48 COPPER (BY SIMILARITY).
FT METAL 63 63 COPPER AND ZINC (BY SIMILARITY).
FT METAL 71 71 ZINC (BY SIMILARITY).
FT METAL 80 80 ZINC (BY SIMILARITY).
FT METAL 83 83 ZINC (BY SIMILARITY).
FT METAL 120 120 COPPER (BY SIMILARITY).
FT DISULFID 57 146 BY SIMILARITY.
FT CARBOHYD 23 23 N-LINKED (GLCNAC...).
SQ SEQUENCE 152 AA; 15732 MW; 4295345C2ADA1203 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
141 GPRP 144

Db

RESULT 31
RS6_AGR15
ID RS6_AGR15 STANDARD; PRT; 153 AA.
AC Q8UG57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S6.

RESULT 32				
SODC NEUCR				
ID SDC NEUCR		STANDARD;	PRT;	153 AA.
AC P07508;				
DT 01-APR-1988				(Rel. 07, Created)
DT 01-AUG-1991				(Rel. 19, Last sequence update)
DT 10-OCT-2003				(Rel. 42, Last annotation update)

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
GN SOB1 OR YUR104C OR J1968.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88263032; PubMed=3290902;
RA Bermingham-McDonogh O., Gralla E., Valentine J.;
RT "The copper, zinc-superoxide dismutase gene of Saccharomyces
RT cerevisiae: cloning, sequencing, and biological activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:4789-4793(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Ramezani Rad M., Kirchrath L., Hollenberg C.P.;
RL Submitted (SEP-1995) to the ENBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE.
RA Johansen J.T., Overballe-Petersen C., Martin B., Hasemann V.,
RA Svendsen I.;
RT "The complete amino acid sequence of copper, zinc superoxide dismutase
RT from Saccharomyces cerevisiae.";
RL Carlsberg Res. Commun. 44:201-217(1979).
RN [4]
RP SEQUENCE.
RX MEDLINE=80227835; PubMed=6993479;
RA Steinman H.M.;
RT "The amino acid sequence of copper-zinc superoxide dismutase from
RT bakers' yeast.";
RL J. Biol. Chem. 255:6758-6765(1980).
RN [5]
RP SEQUENCE OF 1-10.
RC STRAIN=X2180-1A;
RA Frutiger S., Hughes G.J., Sanchez J.-C., Hochstrasser D.F.;
RL Submitted (FEB-1996) to Swiss-Prot.
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92128276; PubMed=1772629;
RA Djinovic K., Gatti G., Coda A., Antolini L., Pelosi G., Desideri A.,
RA Falconi M., Marmocchi F., Rotilio G., Bolognesi M.;
RT "Structure solution and molecular dynamics refinement of the yeast
RT Cu,Zn enzyme superoxide dismutase.";
RL Acta Crystallogr. B 47:918-927(1991).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92292167; PubMed=1602482;
RA Djinovic K., Gatti G., Coda A., Antolini L., Pelosi G., Desideri A.,
RA Falconi M., Marmocchi F., Rotilio G., Bolognesi M.;
RT "Crystal structure of yeast Cu,Zn superoxide dismutase.
RT Crystallographic refinement at 2.5-A resolution.";
RL J. Mol. Biol. 225:791-809(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=99152006; PubMed=10026301;
RA Hart P.J., Balbirnie M.M., Ogihara N.L., Nersissian A.M., Weiss M.S.,
RA Valentine J.S., Eisenberg D.;
RT "A structure-based mechanism for copper-zinc superoxide dismutase.";
RL Biochemistry 38:2167-2178(1999).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
CC -----
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CC -----
CC ENBL; J03279; AAA34543.1; -;
DR EMBL; Z49604; CAA89634.1; -;
DR PIR; A36171; DSBYC.
DR PDB; 1SDY; 31-JAN-94.
DR PDB; 1YSO; 10-JUN-96.
DR PDB; 1JCV; 08-MAR-96.
DR PDB; 2JCM; 08-JUN-99.
DR PDB; 1B4L; 23-DEC-99.
DR PDB; 1B4T; 23-DEC-99.
DR PDB; 1F18; 18-DEC-02.
DR PDB; 1F1A; 18-DEC-02.
DR PDB; 1F1D; 18-DEC-02.
DR PDB; 1F1G; 12-DEC-02.
DR PDB; 1JK9; 05-SEP-01.
DR PDB; 1YAZ; 12-JAN-00.
DR Germonline; 141937; -;
DR SWISS-2DPAGE; P00445; YEAST.
DR SGD; S0003865; SOD1.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0005758; C:mitochondrial intermembrane space; IDA.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IDA.
DR GO; GO:0006878; P:copper ion homeostasis; IGI.
DR GO; GO:0006801; P:superoxide metabolism; IMP.
DR GO; GO:0006882; P:zinc ion homeostasis; IGI.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; sodcu; 1.
DR PRINTS; PR00069; CUZNDISMUTASE.
DR PRODOM; PD000459; SOD_CU_ZN; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; 1.
DR PROSITE; PS00332; SOD_CU_ZN_2; 1.
DR KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc;
KW 3D-structure.
FT INIT MET 0 0
FT METAL 46 46 COPPER.
FT METAL 48 48 COPPER.
FT METAL 63 63 COPPER AND ZINC.
FT METAL 71 71 ZINC.
FT METAL 80 80 ZINC.
FT METAL 83 83 ZINC.
FT METAL 120 120 COPPER.
FT DISULFID 57 146
FT CONFLICT 55 55 N -> D (IN REF. 4).
FT CONFLICT 92 92 N -> D (IN REF. 4).
FT STRAND 2 8
FT STRAND 14 20
FT TURN 24 25
FT STRAND 28 35
FT STRAND 42 48
FT TURN 54 57
FT HELIX 58 60
FT STRAND 63 63
FT TURN 66 67
FT TURN 74 75
FT TURN 81 82
FT STRAND 83 88
FT TURN 91 92
FT STRAND 95 101
FT TURN 109 110
FT TURN 113 114
FT STRAND 116 119
FT TURN 126 127
FT TURN 132 133
FT TURN 134 137
FT HELIX 138 139
FT TURN 145 148
FT STRAND 150 153
SQ SEQUENCE 153 AA; 15723 MW; 4B431A9B5D3211BE CRC64;

Query Match 100.0%; Score 25; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 141 GPRP 144

RESULT 34
NUSB_XYLFA STANDARD; PRT; 157 AA.

ID NUSB_XYLFA STANDARD; PRT; 157 AA.
AC QSPES3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE N utilization substance protein B homolog (NusB protein).
GN NUSB OR XF0955.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=23771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu P.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Pacinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldnan M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Honeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marck C.F.M., Miracca E.C., Miyaki C.V., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nnanl A.Jr., Nobrega P.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
CC -1- FUNCTION: Involved in the transcription termination process (By
CC similarity). Belongs to the nusB family.
CC -1- SIMILARITY: Belongs to the nusB family.
CC
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CC
CC EMBL; AE003934; AAF83765.1; -;
CC PIR; D82741; D82741.
CC HSSP; P04381; 1EY1.
CC DRMAP; MF 00073; -; 1.
CC InterPro; IPR006027; NusB.
CC Pfam; PF01029; NusB; 1.
CC Transcription termination; Complete proteome.

SQ SEQUENCE 157 AA; 17572 MW; 177C94B4EB066169 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 8 GPRP 11

RESULT 35
VG09_HSV11 STANDARD; PRT; 158 AA.

ID VG09_HSV11 STANDARD; PRT; 158 AA.
AC Q00153;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical gene 9 zinc-binding protein.
GN 9.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Ictalurid Herpes-like viruses.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Auburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus";
RL Virology 186:19-14(1992).
CC
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CC
CC EMBL; M75136; AAA88190.1; -;
CC EMBL; M75136; AAA88112.1; -;
CC PIR; A36787; ZBBE11.
CC InterPro; IPR001841; Znf_ring.
CC SMART; SM00184; RING; 1.
CC Hypothetical protein; Zinc; Zinc-finger.
SQ SEQUENCE 158 AA; 17082 MW; BCDB6BC474CEE75E CRC64;

Query Match 100.0%; Score 25; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 131 GPRP 134

RESULT 36
GTR4_CANFA STANDARD; PRT; 162 AA.

ID GTR4_CANFA STANDARD; PRT; 162 AA.
AC Q9XST2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Solute carrier family 2, facilitated glucose transporter, member 4
DE (Glucose transporter type 4, insulin-responsive) (Fragment).
GN SLC2A4 OR GLUT4.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Thyroid;
RX MEDLINE=20422104; PubMed=10964405;
RA Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
RA Christophe D.;
RT "A method for the large-scale cloning of nuclear proteins and nuclear
RT targeting sequences on a functional basis.";
RL Anal. Biochem. 284:231-239(2000).
CC -!- FUNCTION: Insulin-regulated facilitative glucose transporter.
CC -!- SUBUNIT: Binds to DAXX (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Localizes
CC primarily to the perinuclear region, undergoing continued
CC recycling to the plasma membrane where it is rapidly
CC internalized. The dileucine internalization motif is critical
CC for intracellular sequestration (By similarity).
CC -!- PTM: Sumoylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
CC TRANSPORTERS SUBFAMILY.
CC -----
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CC -----
DR EMBL; AJ388533; CAB46835.1; -.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR InterPro; IPR003663; Sugar_transpt.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTNSPORT.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
DR Transmembrane; Sugar transport; Transport; Multigene family.
FT NON_TER 1 1
FT DOMAIN <1 13 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 14 34 8 (POTENTIAL).
FT DOMAIN 35 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 64 9 (POTENTIAL).
FT DOMAIN 65 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 96 10 (POTENTIAL).
FT DOMAIN 97 107 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 108 128 11 (POTENTIAL).
FT DOMAIN 129 135 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 136 156 12 (POTENTIAL).
FT DOMAIN 157 >162 CYTOPLASMIC (POTENTIAL).
FT NON_TER 162 162
SQ SEQUENCE 162 AA; 17453 MW; 0C58CBB23C6AD2BB CRC64;

Query Match 100.0%; Score 25; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
Db 104 GRRP 107

RESULT 37
RR18 ORYSA
ID -RR18 ORYSA STANDARD; PRT; 163 AA.
AC P12152;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chloroplast 30S ribosomal protein S18.
GN RPS18.
OS Oryza sativa (Rice).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=89364698; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiyama M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct rRNA genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL Mol. Gen. Genet. 217:185-194(1989).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the S18P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; X15901; CAA33970.1; -.
DR FTR; JQ0248; R3R218.
DR GRAMME; P12152; -.
DR HAMAP; MF_00270; 1.
DR InterPro; IPR001648; Ribosomal_S18.
DR Pfam; PF01884; Ribosomal_S18; 1.
DR PRINTS; PR00974; RIBOSOMALS18.
DR PRODOM; PD002239; Ribosomal_S18; 1.
DR TIGRFAMs; TIGR00165; S18; 1.
DR PROSITE; PS00057; RIBOSOMAL_S18; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding; Chloroplast; Repeat.
FT DOMAIN 4 52 6 X 7 AA TANDEM REPEATS.
FT REPEAT 4 10
FT REPEAT 11 17
FT REPEAT 18 24
FT REPEAT 25 31
FT REPEAT 32 38
FT REPEAT 39 45
SQ SEQUENCE 163 AA; 19643 MW; 79DA5CB42C125DE5 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
Db 123 GRRP 126

RESULT 38
NKG7 HUMAN
ID -NKG7 HUMAN STANDARD; PRT; 165 AA.
AC Q16617;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein NKG7 (Natural killer cell protein 7) (G-CSF-induced gene 1
DE protein) (Protein GIG-1).
GN NKG7 OR GIG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93209815; PubMed=8458737;
RA Turman M.A., Yabe T., McSherry C., Bach F.H., Houchins J.P.;

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RT "Characterization of a novel gene (NGK7) on human chromosome 19 that
 RT is expressed in natural killer cells and T cells.";
 RL Hum. Immunol. 36:34-40(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94168584; PubMed=7510105;
 RA Shimane M., Tani K., Maruyama K., Takahashi S., Ozawa K., Asano S.;
 RT "Molecular cloning and characterization of G-CSF induced gene cDNA.";
 RL Biochem. Biophys. Res. Commun. 199:26-32(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Church R.L., Li X.L., Wang J.H.;
 RT "Human chromosome 19q13.4 DNA sequence, including complete sequence
 RT for LIM2 and NGK7.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Raheij J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc Natl Acad Sci U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in activated T cells, in kidney,
 CC liver, lung and pancreas. Not expressed in brain, heart, or
 CC skeletal muscle. Expressed at high levels in TCR gamma delta-
 CC expressing CTL clones, and in some TCR alpha beta-expressing CTL
 CC clones (both CD4+ and CD8+), but is not expressed in other TCR
 CC alpha beta-expressing CTL clones and in cell lines representing B
 CC cells, monocytes, and myeloid cells.
 CC -!- INDUCTION: By G-CSF.
 CC -!- SIMILARITY: Belongs to the PMP-22 / BMP / MP20 family.
 CC
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 CC
 CC ENBL; U09608; AAA18209.1; -;
 CC ENBL; S83115; AAB30078.1; -;
 CC ENBL; AF05941; AAG32329.1; -;
 CC ENBL; BC015759; AAH15759.1; -;
 CC PIR; JC2081; JC2081.
 CC Genew; HGNC:7830; NGK7.
 CC MIM; 606008; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC InterPro; IPR004031; PMP22_Claudin.
 CC InterPro; IPR004032; PMP22_EMP_MP20.
 CC Pfam; PF00822; PMP22_Claudin; 1.
 CC PROSITE; PS01221; PMP22_1; FALSE_NEG.
 CC PROSITE; PS01222; PMP22_2; FALSE_NEG.
 KW Transmembrane.
 FT TRANSMEM 9 29 POTENTIAL.

FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 92 112 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 SQ SEQUENCE 165 AA; 17664 MW; CEE2901B6DC42A8C CRC64;
 Query Match 100.0%; Score 25; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 1 GPRP 4
 DB 157 GPRP 160
 RESULT 39
 FGFM HUMAN STANDARD; PRT; 170 AA.
 ID FGFM HUMAN
 AC OHCTO;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibroblast growth factor-22 precursor (FGF-22) (UNQ2500/PRO5800).
 GS FGF22.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=21240339; PubMed=11342227;
 RA Nakatani Y., Hoshikawa M., Asaki T., Kassai Y., Itoh N.;
 RT "Identification of a novel fibroblast growth factor, FGF-22,
 RT preferentially expressed in the inner root sheath of the hair
 RT follicle.";
 RL Biochim. Biophys. Acta 1517:460-463(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2287296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chul C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wileand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 CC -!- FUNCTION: May be involved in hair development.
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC
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 CC
 CC ENBL; AB021925; BAB13479.1; -;
 CC ENBL; AY359084; AAQ89955.1; -;
 CC HSSP; P31371; IG82
 CC Genew; HGNC:3679; FGF22.
 CC MIM; 605831; -;
 CC GO; GO:0005615; C:extracellular space; NAS.
 CC GO; GO:0030154; P:cell differentiation; NAS.
 CC InterPro; IPR008996; Cytok III-like.
 CC InterPro; IPR002348; III_HBGF.


```

RT "Purification and structural characterization of bovine
RL cathelicidins, precursors of antimicrobial peptides."
RL Eur. J. Biochem. 238:769-776(1996).
CC -!- FUNCTION: Exerts, in vitro, a potent antimicrobial activity.
CC Probably due to an impairment of the function of the respiratory
CC chain and of energy-dependent activities in the inner membrane
CC of susceptible microorganisms.
CC -!- TISSUE SPECIFICITY: Large granules of neutrophils.
CC -!- PTM: Elastase is responsible for its maturation.
CC -!- MASS SPECTROMETRY: MW=18395; MW_ERR=1; METHOD=Electrospray;
CC RANGE=30-130.
CC -!- SIMILARITY: Belongs to the cathelicidin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L42977; AAA87359.1; -
CC EMBL; Y09471; CAA70616.1; -
CC InterPro; IPR001894; Cathelicidin.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidins; 1.
CC ProSITE; PS00946; CATHELICIDINS; 1.
CC ProSITE; PS00947; CATHELICIDINS; 2.
CC Antibiocic; Repeat; Signal; Pyrrolidone carboxylic acid.
CC SIGNAL 1 29 POTENTIAL.
CC PROPEP 30 130
CC PEPTIDE 131 190
CC PROPEP 189 190
CC MOD_RES 30 30
CC DISULFID 85 96
CC DISULFID 107 124
CC SS SEQUENCE 190 AA; 21567 MW; 8CD07D7AA30A731C CRC64;

Query Match 100.0%; Score 25; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 154 GPRP 157

RESULT 42
AP10_ARATH STANDARD; PRT; 192 AA.
AC Q92PW2; Q8L8L8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Anaphase promoting complex subunit 10 (AP10) (Cyclosome subunit 10).
GN AT2G18290 OR T30D6.20.
CS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Unayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrara A.J., Creasy T.H.,
RA Goodman H.M., Schmerville C.R., Copenhagen G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;

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RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RL thaliana."
RL Nature 402:761-768(1999).
CC [2]
CC SEQUENCE FROM N.A.
CC Brover V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell R.,
CC Feldmann K.A.;
CC "Full-length cDNA from Arabidopsis thaliana."
CC Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Component of the anaphase promoting complex/cyclosome
CC (APC/C), a cell cycle-regulated ubiquitin ligase that controls
CC progression through mitosis and the G1 phase of the cell cycle (By
CC similarity).
CC -!- SUBUNIT: The APC is composed of at least 11 subunits (By
CC similarity).
CC -!- SIMILARITY: Belongs to the APC10 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AC006439; AAD15507.2; -
CC EMBL; AY087130; AAM64688.1; -
CC InterPro; IPR004939; APC10.
CC Pfam; PF03256; APC10; 1.
CC Ubl conjugation pathway; Cell cycle; Mitosis.
CC CONFLICT 112 112 E -> D (IN REF. 2).
CC SEQUENCE 192 AA; 21750 MW; 5ADBE08F7D12FFC CRC64;

Query Match 100.0%; Score 25; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 167 GPRP 170

RESULT 43
RNF4_MOUSE STANDARD; PRT; 194 AA.
AC Q9QZS2; Q35941;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING finger protein 4.
GN RNF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Embryo;
RX MEDLINE=20284895; PubMed=10822263;
RA Galili N., Nayak S., Epstein J.A., Buck C.A.;
RA "Rnf4, a RING protein expressed in the developing nervous and
RT reproductive systems, interacts with Gsc1, a gene within the DiGeorge
RT critical region."
RL Dev. Dyn. 218:102-111(2000).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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RA Fleischmann M., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okado T., Furuno M., Anon H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Washima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
RA Hayashizaki Y.,
RT Functional annotation of a full-length mouse cDNA collection.;
RN Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [4]
RP SEQUENCE OF 16-178 FROM N.A.
RX TISSUE=Embryo;
RC MEDLINE=98140125; PubMed=9479498;
RA Chiarotti L., Benvenuto G., Fedele M., Santoro M., Simone A.,
RA Fusco A., Bruni C.B.;
RT "Identification and characterization of a novel RING-finger gene
(RNF4) mapping at 4p16.3.";
RL Genomics 47:258-265(1998).
RN [5]
RP INTERACTION WITH TCF20.
RX MEDLINE=20408957; PubMed=10849425;
RA Lygsoe C., Bouteiller G., Dangaard C.K., Ryom D., Sanchez-Munoz S.,
RA Noerby P.L., Bonven B.J., Joergensen P.;
RT "Interaction between the transcription factor SPBP and the positive
cofactor RNF4. An interplay between protein binding zinc fingers.";
RL J. Biol. Chem. 275:26144-26149(2000).
CC -!- FUNCTION: Enhances steroid receptor-mediated transcriptional
activation as well as activating basal transcription (By
similarity).
CC -!- SUBUNIT: Interacts with GSK3, Androgen receptor, TCF20, TBP and
ZNF278.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: In the embryo, expressed primarily in the
developing nervous system with strong expression in the dorsal
root ganglia and gonads. Ubiquitously expressed in the adult.
CC -!- DEVELOPMENTAL STAGE: Expression is detected from embryonic day 7
and continues throughout development and into adulthood.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -----
DR EMBL; AF169300; AAF00620.1; -
DR EMBL; AK019171; BAB31585.1; -
DR EMBL; BC003282; AAH03282.1; -
DR EMBL; U95141; AAC53539.1; -
DR MGD; MGI:1201691; Rnf4; -
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Transcription regulation, Activator, Zinc-finger; Nuclear protein.
FT ZN FING 135 181
FT RING-TYPE
SQ SEQUENCE 194 AA; 21910 MW; 9A0A4277725C62E5 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
DB 127 GRRP 130

RESULT 44
KGUA HUMAN STANDARD; PRT; 196 AA.
ID KGUA_HUMAN
AC Q16774; Rel. 35, Created
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Guanylate kinase (EC 2.7.4.8) (GMP kinase).
GN GUK1 OR GUK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96213684; PubMed=8647247;
RA Fitzgibbon J., Katsanis N., Wells D., Delhanty J., Vallins W.,
RA Hunt D.M.;
RT "Human guanylate kinase (GUK1): cDNA sequence, expression and
chromosomal localization.";
RL FEBS Lett. 385:185-188(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96279248; PubMed=8663313;
RA Brady W.A., Kokoris M.S., Fitzgibbon M., Black M.E.;
RT "Cloning, characterization, and modeling of mouse and human guanylate
kinases.";
RL J. Biol. Chem. 271:16734-16740(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Essential for recycling GMP and indirectly, cGMP.
 CC -!- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the guanylate kinase family.
 CC
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 CC
 CC EMBL: L76200; AAC37598.1; -.
 CC EMBL: U66895; AAC50659.1; -.
 CC EMBL: BC006249; AAH06249.1; -.
 CC EMBL: BC009914; AAH09914.1; -.
 CC PIR: S68864; S68864.
 CC HSSP: P15454; IGKY.
 CC Genew: HGNC:4693; GUK1.
 CC MIM: 139270; -.
 CC GO: GO:0004385; P:guanylate kinase activity; TAS.
 CC GO: GO:0006183; P:GTP biosynthesis; TAS.
 CC InterPro: IPR008143; Guanylate_kin.
 CC InterPro: IPR008144; Guanylate_kin.
 CC Pfam: PF00625; Guanylate_kin; 1.
 CC SMART: SM00072; GUKC; 1.
 CC PROSITE: PS00856; GUANYLATE_KINASE_1; 1.
 CC PROSITE: PS00852; GUANYLATE_KINASE_2; 1.
 CC TRANSFERASE; Kinase; ATP-binding; Acetylation.
 CC INIT MET 0 BY SIMILARITY.
 CC NP BIND 10 17 ATP (BY SIMILARITY).
 CC MOD RES 1 1 ACETYLATION (BY SIMILARITY).
 CC SEQUENCE 196 AA; 21594 MW; C4727A7E2AA261B3 CRC64;
 CC
 CC Query Match 100.0%; Score 25; DB 1; Length 196;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 GPRP 4
 CC Db 2 GPRP 5
 CC
 CC RESULT 45
 CC KGUA BOVIN STANDARD; PRT; 197 AA.
 CC AC P46135;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Guanylate kinase (EC 2.7.4.8) (GMP kinase).
 CC GUK1 OR GUK.
 CC OS Bos taurus (Bovine).
 CC CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC CC Bovidae; Bovinae; Bos.
 CC CC NCBI_TaxID=9913;
 CC CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RC TISSUE=Retina;
 CC RA MEDLINE=94271265; PubMed=7911663;
 CC RA Gaiderov I.O., Suslov O.N., Ovchinnikova T.V., Abdulaev N.G.;
 CC "Guanylate kinase from bovine retina: isolation, primary structure, and expression in E. coli.";
 CC Bioorg. Khim. 20:367-381 (1994).
 CC -!- FUNCTION: Essential for recycling GMP and indirectly, cGMP.
 CC

CC -!- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the guanylate kinase family.
 CC
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 CC
 CC EMBL: X67029; CAA47423.1; -.
 CC PIR: S39447; S39447.
 CC HSSP: P15454; IGKY.
 CC InterPro: IPR008144; Guanylate_kin.
 CC InterPro: IPR008145; Guanylt/Ca.
 CC Pfam: PF00625; Guanylate_kin; 1.
 CC SMART: SM00072; GUKC; 1.
 CC PROSITE: PS00856; GUANYLATE_KINASE_1; 1.
 CC PROSITE: PS00852; GUANYLATE_KINASE_2; 1.
 CC TRANSFERASE; Kinase; ATP-binding; Acetylation.
 CC INIT MET 0 BY SIMILARITY.
 CC NP BIND 10 17 ATP (BY SIMILARITY).
 CC MOD RES 1 1 ACETYLATION (BY SIMILARITY).
 CC SEQUENCE 197 AA; 21778 MW; 5CB3DD007BC15C62 CRC64;
 CC
 CC Query Match 100.0%; Score 25; DB 1; Length 197;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 GPRP 4
 CC Db 2 GPRP 5
 CC
 CC RESULT 46
 CC KGUA MOUSE STANDARD; PRT; 197 AA.
 CC AC Q64520;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Guanylate kinase (EC 2.7.4.8) (GMP kinase).
 CC GUK1 OR GWK.
 CC OS Mus musculus (Mouse).
 CC CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC CC NCBI_TaxID=10090;
 CC CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RP MEDLINE=96279248; PubMed=8663313;
 CC RA Brady W.A., Kokoris M.S., Fitzgibbon M., Black M.E.;
 CC "Cloning, characterization, and modeling of mouse and human guanylate kinases";
 CC J. Biol. Chem. 271:16734-16740 (1996).
 CC -!- FUNCTION: Essential for recycling GMP and indirectly, cGMP.
 CC -!- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the guanylate kinase family.
 CC
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 CC
 CC EMBL: U53514; AAC52652.1; -.
 CC FDB: ILVG; 11-DEC-02.
 CC MGD: MGI:95871; Guk1.
 CC InterPro: IPR008144; Guanylate_kin.

DR InterPro; IPR008145; Guanylt/Ca.
DR Pfam; PF00625; Guanylate_kin; 1.
DR SMART; SM00072; GuK; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS00552; GUANYLATE_KINASE_2; 1.
KW Transferase; Kinase; ATP-binding; Acetylation; 3D-structure.
FT INIT_WET 0 BY SIMILARITY.
FT NP_BIND 10 17 ATP (BY SIMILARITY).
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 197 AA; 21787 MW; 332403BF0D1CCFB2 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
D 2 GPRP 5
Db 146 GPRP 149

RESULT 47
GDIS_BOVIN
ID GDIS_BOVIN STANDARD; PRT; 200 AA.
AC Q9TU03;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)
DE (D4-GDP-dissociation inhibitor) (D4-GDI).
GN ARHGDI2 OR GDI4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN RFLX
RP MEDLINE=20264070; PubMed=10802295;
RA Davis A.R., Clements M.K., Burger P.L., Siemsen D.W., Quinn M.T.;
RT "Cloning of bovine low molecular weight GTPases (Rac1 and Rac2) and
RL Rho GDP-dissociation inhibitor 2 (D4-GDI).";
RL Vet. Immunol. Immunopathol. 74:285-301(2000).
CC -!- FUNCTION: Regulates the GDP/GTP exchange reaction of the Rho
CC proteins by inhibiting the dissociation of GDP from them, and the
CC subsequent binding of GTP to them.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the Rho GDI family.
CC
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CC
CC EMBL; AF182001; AAF00938.1; -.
DR HSSP; P52566; IDS6.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000406; Rho GDI.
DR Pfam; PF02115; RhoGDI; 1.
DR PRINTS; PR00492; RHOGDI.
KW GTPase activation.
SQ SEQUENCE 200 AA; 22794 MW; E89F1E38993AFDE5 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
D 2 GPRP 5
Db 146 GPRP 149

RESULT 48
GDIS_MOUSE
ID GDIS_MOUSE STANDARD; PRT; 200 AA.
AC Q61559;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (D4).
DE ARHGDI2 OR GDI4.
GN ARHGDI2 OR GDI4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN RFLX
RP MEDLINE=10090;
RA [1]
RT SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss;
RX MEDLINE=94206871; PubMed=7512369;
RA Adra C.N., Ko J., Leonard D., Wirth L.J., Cerione R.A., Lim B.;
RT "Identification of a novel protein with GDP dissociation inhibitor
RT activity for the ras-like proteins CDC42Hs and rac 1.";
RL Genes Chromosomes Cancer 8:253-261(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=1247732;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Regulates the GDP/GTP exchange reaction of the Rho
CC proteins by inhibiting the dissociation of GDP from them, and the
CC subsequent binding of GTP to them.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Preferentially expressed in hematopoietic
CC cells.
CC -!- SIMILARITY: Belongs to the Rho GDI family.
CC
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CC
CC EMBL; L07918; AAA61613.1; -.
DR EMBL; BC031763; AAH31763.1; -.
DR PIR; I49687; I49687.
DR HSSP; P52566; IDS6.
DR PNMA-2DPAGE; Q51599; -.
DR MCD; MGI:101940; Arhgdib.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000406; Rho GDI.
DR Pfam; PF02115; Rho GDI; 1.
DR PRINTS; PR00492; RHOGDI.
KW GTPase activation.

SQ SEQUENCE 200 AA; 22851 MW; EA78C965FIAB6F5C CRC64;
 Query Match 100.0%; Score 25; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPRP 4
 Db 146 GPRP 149

RESULT 49
 ID -GDI5 HUMAN STANDARD; PRT; 201 AA.
 AC P25266; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI).
 GN ARHGDI2 OR GDI2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RN R1
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93361488; PubMed=8356058;
 RA Scherle P., Behrens T., Staudt L.M.;
 RT "Ly-GDI, a GDP-dissociation inhibitor of the RhoA GTP-binding
 RT protein, is expressed preferentially in lymphocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7568-7572(1993).
 [2]
 RN R2
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94085490; PubMed=8262133;
 RA Leffers H., Nielsen M.S., Andersen A.H., Honore B., Madsen P.,
 RA Vandekerckhove J., Celis J.E.;
 RT "Identification of two human Rho GDP dissociation inhibitor proteins
 RT whose overexpression leads to disruption of the actin cytoskeleton";
 RL Exp. Cell Res. 209:165-174(1993).
 [3]
 RN R3
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93165719; PubMed=8434008;
 RA Leillas J.M., Adra C.N., Wulf G.M., Guilleminot J.C., Caput D.,
 RA Lim B.;
 RT "cDNA cloning of a human mRNA preferentially expressed in
 RT hematopoietic cells and with homology to a GDP-dissociation inhibitor
 RT for the rho GTP-binding proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1479-1483(1993).
 [4]
 RN R4
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max A.M., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RN R5
 RP X-RAY CRYSTALLOGRAPHY (2.35 ÅNGSTROMS) OF COMPLEX WITH RAC2.
 RX MEDLINE=20122627; PubMed=10655644;
 RA Scheffzek K., Stephan I., Jensen C.N., Ilienberger D., Gierschik P.;
 RT "The Rac-RhoGDI complex and the structural basis for the regulation
 RT of Rho proteins by RhoGDI.";
 RL Nat. Struct. Biol. 7:122-126(2000).
 CC -!- FUNCTION: Regulates the GDP/GTP exchange reaction of the Rho
 CC proteins by inhibiting the dissociation of GDP from them, and the
 CC subsequent binding of GTP to them.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the Rho GDI family.
 CC -----
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 CC -----
 CC EMBL: L20688; AAA59539.1; -;
 DR EMBL: X69549; CAA49280.1; -;
 DR EMBL: L07916; -; NOT_ANNOTATED_CDS.
 DR EMBL: AF498927; AA021075.1; -;
 DR EMBL: BC009200; AA09200.1; -;
 DR PIR: A47742; A47742.
 DR PDB: 1DS6; 19-JUL-00.
 DR Aarhus/Ghent-2DPAGE; 8120; IEF.
 DR Aarhus/Ghent-2DPAGE; 1120; IEF.
 DR Genew; HGNC:679; ARHGDI2.
 DR MIM: 602843; -;
 DR GO: 0016023; C:cytoplasmic vesicle; TAS.
 DR GO: 0005094; F:Rho GDP-dissociation inhibitor activity; TAS.
 DR GO: 0030036; P:actin cytoskeleton organization and biogenesis; TAS.
 DR GO: 0007275; P:development; TAS.
 DR GO: 0006955; P:immune response; TAS.
 DR GO: 0007162; P:negative regulation of cell adhesion; TAS.
 DR GO: 0007266; P:Rho protein signal transduction; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR004046; Rho GDI.
 DR Pfam; PF02115; Rho GDI; I.
 DR PRINTS; PR00492; RHGDI.
 DR GTPase activation; 3D-structure.
 KW CONFLICT 169 170 RG -> QD (IN REF. 3).
 FT HELIX 32 37
 FT TURN 38 41
 FT HELIX 43 52
 FT TURN 53 53
 FT STRAND 59 75
 FT TURN 77 78
 FT TURN 84 86
 FT TURN 87 88
 FT HELIX 91 96
 FT STRAND 98 102
 FT TURN 103 104
 FT STRAND 106 113
 FT STRAND 120 131
 FT TURN 132 133
 FT STRAND 134 146
 FT STRAND 153 156
 FT STRAND 160 161
 FT TURN 166 168
 FT STRAND 170 179
 FT TURN 181 182
 FT TURN 187 196
 SQ SEQUENCE 201 AA; 22988 MW; F1E840134F643B5F CRC64;

Search completed: September 7, 2004, 18:58:47
Job time : 25 secs

Query Match 100.0%; Score 25; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 147 GPRP 150

RESULT 50

YK86 MYCTU STANDARD; PRT; 201 AA.
AC Q10634;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Very Hypothetical protein RV2086/MB2113.
GN RV2086 OR MTCY49.27 OR MB2113.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]

SEQUENCE FROM N.A.
RP SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=3634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala E.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares R., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]

SEQUENCE FROM N.A.
RP SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duchoy S., Grondin S., Iacrolx C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -!- SIMILARITY: SOME, TO TRANSPOSASES.

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CC -----

DR EMBL; Z73966; CAA98198.1; ALT INIT.
DR EMBL; BX248341; CAD96966.1; -.
DR Tuberculist; RV2086;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 201 AA; 22518 MW; 22AEC2268708FESB CRC64;

Query Match 100.0%; Score 25; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 131 GPRP 134

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OM protein - protein search, using sw model
Run on: September 7, 2004, 18:52:52 ; Search time 115 Seconds
(without alignments)
10.975 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_todent.*

12: sp_virus.*

13: sp_vertibrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	27	11 Q99KX5	Q99KX5 mus musculus
2	25	100.0	31	4 Q9BYV4	Q9BYV4 homo sapien
3	25	100.0	36	12 Q91CY3	Q91CY3 tt virus. o
4	25	100.0	43	2 Q9BYJ2	Q9BYJ2 streptococc
5	25	100.0	44	4 Q8TCB9	Q8TCB9 homo sapien
6	25	100.0	50	10 Q7X128	Q7X128 oryza sativ
7	25	100.0	51	12 Q8QPT9	Q8QPT9 tomato chlo
8	25	100.0	52	4 Q9UNX8	Q9UNX8 homo sapien
9	25	100.0	53	5 Q9V8Y1	Q9V8Y1 drosophila
10	25	100.0	56	11 Q9CSQ6	Q9CSQ6 mus musculu
11	25	100.0	56	15 Q856S5	Q856S5 murine leuk
12	25	100.0	57	11 Q61460	Q61460 mus musculu
13	25	100.0	57	16 Q8VKP1	Q8VKP1 mycobacteri
14	25	100.0	65	5 Q9W3Q8	Q9W3Q8 drosophila
15	25	100.0	66	5 Q18234	Q18234 caenorhabdi
16	25	100.0	67	3 Q9US68	Q9US68 schizosacch

17	25	100.0	67	5 Q23727	Q23727 chironomus
18	25	100.0	67	11 Q54493	Q54493 mus musculu
19	25	100.0	69	5 Q23725	Q23725 chironomus
20	25	100.0	69	10 Q8H408	Q8H408 oryza sativ
21	25	100.0	70	10 Q9MAV4	Q9MAV4 arabidopsis
22	25	100.0	70	17 Q8TJTO	Q8TJTO methanosarc
23	25	100.0	71	2 Q93M44	Q93M44 bordetella
24	25	100.0	72	5 Q9XWV3	Q9XWV3 caenorhabdi
25	25	100.0	73	11 Q8QYF1	Q8QYF1 rattus norv
26	25	100.0	73	12 Q86984	Q86984 galleria me
27	25	100.0	74	2 Q847P0	Q847P0 aster yello
28	25	100.0	74	10 Q9M3Q3	Q9M3Q3 hordeum bul
29	25	100.0	76	4 Q9P1C0	Q9P1C0 homo sapien
30	25	100.0	76	4 Q00397	Q00397 homo sapien
31	25	100.0	76	5 Q9VF98	Q9VF98 drosophila
32	25	100.0	77	4 Q9NRK3	Q9NRK3 homo sapien
33	25	100.0	77	16 Q98A78	Q98A78 rhizobium l
34	25	100.0	77	16 Q89YC1	Q89YC1 bradyrhizob
35	25	100.0	78	16 Q81MP0	Q81MP0 bacillus an
36	25	100.0	79	5 Q23726	Q23726 chironomus
37	25	100.0	80	10 Q81534	Q81534 saccharum o
38	25	100.0	81	6 Q9N0U0	Q9N0U0 bubalus bub
39	25	100.0	82	12 Q8QY94	Q8QY94 tt virus. o
40	25	100.0	83	12 Q81845	Q81845 hepatitis d
41	25	100.0	83	12 Q81839	Q81839 hepatitis d
42	25	100.0	84	6 Q8HY00	Q8HY00 callithrix
43	25	100.0	84	12 Q67593	Q67593 miscanthus
44	25	100.0	84	12 Q72913	Q72913 miscanthus
45	25	100.0	86	16 Q98AH9	Q98AH9 rhizobium l
46	25	100.0	86	16 Q9ADA9	Q9ADA9 streptomyce
47	25	100.0	87	2 Q845Q9	Q845Q9 aeromonas s
48	25	100.0	87	12 P87913	P87913 human herpe
49	25	100.0	87	12 Q39500	Q39500 bovine herp
50	25	100.0	87	16 Q9CBF6	Q9CBF6 mycobacteri
51	25	100.0	88	10 Q7XDU1	Q7XDU1 oryza sativ
52	25	100.0	88	16 Q92RU0	Q92RU0 rhizobium m
53	25	100.0	88	16 Q98XN5	Q98XN5 bradyrhizob
54	25	100.0	88	16 Q81PL2	Q81PL2 bacillus an
55	25	100.0	90	4 Q87AH8	Q87AH8 homo sapien
56	25	100.0	90	16 Q8YDX9	Q8YDX9 bruceella me
57	25	100.0	90	16 Q9X847	Q9X847 streptomyce
58	25	100.0	91	2 Q9ETR6	Q9ETR6 lactobacill
59	25	100.0	91	2 Q9EVJ4	Q9EVJ4 lactobacill
60	25	100.0	91	2 Q9EUA4	Q9EUA4 lactobacill
61	25	100.0	91	12 Q8QY95	Q8QY95 tt virus. o
62	25	100.0	91	16 Q8U876	Q8U876 agrobacteri
63	25	100.0	92	12 Q05614	Q05614 human herpe
64	25	100.0	92	17 Q9VAL1	Q9VAL1 aeropyrum p
65	25	100.0	93	10 Q8S2D8	Q8S2D8 oryza sativ

ALIGNMENTS

RESULT 1				
Q99KX5	ID	Q99KX5	PRELIMINARY;	PRT; 27 AA.
AC	Q99KX5	Q99KX5	Q99KX5 mus musculu	
DT	01-JUN-2001	(TEMBLrel. 17, Created)		
DT	01-JUN-2001	(TEMBLrel. 17, Last sequence update)		
DT	01-OCT-2003	(TEMBLrel. 25, Last annotation update)		
DB	Hypothetical protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
[1]	SEQUENCE FROM N.A.			
RP	Strausberg R.;			
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC003968; AA03968.1; -			
DR	Hypothetical protein.			
KW	Hypothetical protein.			
SQ	SEQUENCE 27 AA; 2832 MW; 4008F368AF868B63 CRC64;			

Query Match 100.0%; Score 25; DB 11; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 19 GPRP 22

RESULT 2
 Q9BVY4 PRELIMINARY; PRT; 31 AA.
 ID Q9BVY4
 AC Q9BVY4
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC000821; AA00821.1; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 31 AA; 3570 MW; E501FCF1DC4CB889 CRC64;

Query Match 100.0%; Score 25; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 4 GPRP 7

RESULT 3
 Q91CY3 PRELIMINARY; PRT; 36 AA.
 ID Q91CY3
 AC Q91CY3
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF1 (Fragment).
 OS TT virus.
 OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
 ON NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Saa-07;
 RX MEDLINE=2148821; PubMed=11601907;
 RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
 RA Yoshikawa A.;
 RT "Heterogeneous distribution of TT virus of distinct genotypes in
 RT multiple tissues from infected humans."
 RL Virology 288:358-368(2001).
 DR ENBL; AB060599; BAB69922.1; -;
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 3878 MW; 875464E84E3A2A69 CRC64;

Query Match 100.0%; Score 25; DB 12; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 19 GPRP 22

RESULT 4
 Q9EXJ2 PRELIMINARY; PRT; 43 AA.
 ID Q9EXJ2
 AC Q9EXJ2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Priming glycosyltransferase (Fragment).
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 ON NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FYE-41;
 RA Provencher C., Sirois S., Lapointe G., Roy D.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF323531; AAC38624.1; -;
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR003362; Bact_transf.
 DR Pfam; PF02397; Bact_transf. 1.
 KW Transferase.
 FT NON_TER 1
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 4875 MW; 85DD21E6A95BA5DA CRC64;

Query Match 100.0%; Score 25; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 14 GPRP 17

RESULT 5
 Q8TCB9 PRELIMINARY; PRT; 44 AA.
 ID Q8TCB9
 AC Q8TCB9
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022395; AA022395.1; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 44 AA; 4753 MW; 9F95AA5A14D0DDF3 CRC64;

Query Match 100.0%; Score 25; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 34 GPRP 37

RESULT 6
 Q7X128 PRELIMINARY; PRT; 50 AA.
 ID Q7X128
 AC Q7X128;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Hypothetical protein P0506C07.3.
 GN P0506C07.3.
 OS Oryza sativa (japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Eriatoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GN3) genomic DNA, chromosome 7, PAC
 clone:P0506C07.3";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004384; BAC79929.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 50 AA; 5492 MW; B13B993B842B80DF CRC64;

 Query Match 100.0%; Score 25; DB 10; Length 50;
 Best Local Similarity 100.0%; Pred. No. 4.e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GPRP 4
 DB 3 GPRP 6

 RESULT 7
 Q8QPT9 PRELIMINARY; PRT; 51 AA.
 ID Q8QPT9
 AC Q8QPT9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Capsid protein (Fragment).
 GN AV1.
 OS Tomato chlorotic mottle virus.
 CC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=172391;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RJ-Sf1;
 RA Ribeiro S.G., Ambrozovic L.P., de Avila A.C., Calegario R.F.,
 RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
 RT "Distribution and genetic diversity of tomato-infecting geminiviruses
 in Brazil";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY049209; AAL62835.1; -.
 FT NON TER 51
 SQ SEQUENCE 51 AA; 5875 MW; 8C605E978E2F2758 CRC64;

 Query Match 100.0%; Score 25; DB 12; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GPRP 4
 DB 30 GPRP 33

 RESULT 8
 Q9UNX8 PRELIMINARY; PRT; 52 AA.
 ID Q9UNX8
 AC Q9UNX8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome P450 (Fragment).
 GN CYP2B6.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99156873; PubMed=10037683;
 RX Sueyoshi T., Kawamoto T., Zelko I., Honkakoaki P., Negishi M.;
 RT "The repressed nuclear receptor CAR responds to phenobarbital in
 activating the human CYP2B6 gene";
 RL J. Biol. Chem. 274:6043-6046(1999).
 DR EMBL; AF081569; AAD25924.1; -.
 DR GO; GO:006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 FT NON TER 52
 SQ SEQUENCE 52 AA; 5846 MW; 67933CB4DC69B76E CRC64;

 Query Match 100.0%; Score 25; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GPRP 4
 DB 33 GPRP 36

 RESULT 9
 Q9V8Y1 PRELIMINARY; PRT; 53 AA.
 ID Q9V8Y1
 AC Q9V8Y1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG15126 protein.
 GN CG15126.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Beckley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Adair J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR ENBL: AE003795; AAF57523.1; --
 DR FlyBase; FBgn040729; CG15126.
 SQ SEQUENCE 53 AA; 5388 MW; 68828750C9C82142 CRC64;

Query Match 100.0%; Score 25; DB 5; Length 53;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 42 GPRP 45

RESULT 10
 Q9CSQ6 PRELIMINARY; PRT; 56 AA.
 AC Q9CSQ6
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cyclin-dependent kinase 4 (Fragment).
 GN CDK4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SQ SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayaishizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR ENBL, AK012202; BAB28096.1; --
 DR MGD; MGI:88357; CDK4.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005667; C:transcription factor complex; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0004672; F:protein kinase activity; IDA.
 DR GO; GO:0007165; P:signal transduction; IDA.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF00069; pkinase; I.
 DR ATP-binding; Transferase.
 FT NON TER 1 1
 SQ SEQUENCE 56 AA; 6347 MW; 3BF3E61D689B04CD CRC64;

Query Match 100.0%; Score 25; DB 11; Length 56;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 6 GPRP 9

RESULT 11
 Q85655 PRELIMINARY; PRT; 56 AA.
 AC Q85655
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag p10 protein.
 OS Murine leukemia virus.
 OC Viruses; Retroviruses; Retroviridae; Gammaretrovirus.
 OX NCBI_TaxID=11786;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Duplan MuLV;
 RX MEDLINE=89181946; PubMed=2538760;
 RA Aziz D.C., Jolicoeur P., Zaher H.,
 RT "Severe immunodeficiency disease induced by a defective Murine leukemia virus."
 RL Nature 338:505-508(1989).
 DR ENBL; X14576; CAA32719.1; --
 DR GO; GO:0019012; C:virus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; I.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; I.
 DR PROSITE; PS0158; ZF_CCHC; I.
 KW Core protein; Polyprotein.
 SQ SEQUENCE 56 AA; 6387 MW; 4C2C72DFCC12FBA3 CRC64;

Query Match 100.0%; Score 25; DB 15; Length 56;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 48 GPRP 51

RESULT 12
 Q61460 PRELIMINARY; PRT; 57 AA.
 ID Q61460
 AC Q61460
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Testosterone 16a-hydroxylase type c (Fragment).
 GN CYP2B13 OR 16AHC-C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91146586; PubMed=1997326;
 RA Lakso M., Masaki R., Noshiro M., Negishi M.,
 RT "Structures and characterization of sex-specific mouse cytochrome P-450 genes as members within a large family. Duplication boundary and evolution."
 RL Eur. J. Biochem. 195:477-486(1991).
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR ENBL; M60359; AAA03650.1; --
 DR PIR; I49627; I49627.
 DR MGD; MGI:88599; Cyp2b13.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; p450; I.

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KW Heme; Monooxygenase; Oxidoreductase.
FT NON TER 57
SQ SEQUENCE 57 AA; 6311 MW; 3FF9AA1979283DB9 CRC64;

Query Match 100.0%; Score 25; DB 11; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 33 GPRP 36

RESULT 13
ID Q8VKP1 PRELIMINARY; PRT; 57 AA.
AC Q8VKP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein MT0290.
GN MT0290.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Unayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE006936; AAK44510.1; -.
DR TIGR; MT0290; -.
KW Hypothetical protein.
SQ SEQUENCE 57 AA; 6035 MW; BECA0B080B62690A CRC64;

Query Match 100.0%; Score 25; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 30 GPRP 33

RESULT 14
ID Q9W3Q8 PRELIMINARY; PRT; 65 AA.
AC Q9W3Q8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG11368 protein (RH67809p).
GN CG11368.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Geisel C., Stellyes L., Bradshaw H.;
 RT "The sequence of *C. elegans* cosmid C26F1.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U53148; AAB37072.2; -;
 DR PIR; T15646; T15646.
 DR WormPep; C26F1.10; CE30733.
 KW Hypothetical protein.
 SQ SEQUENCE 66 AA; 7486 MW; 822065216CB30F9F CRC64;

Query Match 100.0%; Score 25; DB 5; Length 66;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
 Db 59 GRRP 62

RESULT 16

Q9US68 PRELIMINARY; PRT; 67 AA.
 AC Q9US68;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical nuclear protein (Fragment).
 GN SPBC887.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=968 h90.
 RX MEDLINE=20232868; PubMed=10759889;
 RA Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Harauchi T.,
 RA Hiraoka Y.;
 RT "Large-scale screening of intracellular protein localization in living
 RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
 RL Genes Cells 5:169-190(2000).
 DR EMBL; A8028010; BAA87314.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR Nuclear protein.
 KW Nuclear protein.
 FT NON TER 1
 FT NON TER 67
 SQ SEQUENCE 67 AA; 7580 MW; DBD818EF169DF280 CRC64;

Query Match 100.0%; Score 25; DB 3; Length 67;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
 Db 60 GRRP 63

RESULT 17

Q23727

ID Q23727 PRELIMINARY; PRT; 67 AA.
 AC Q23727;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Balbiani ring 2 (BR2) gene (Fragment).
 OS Chironomus pallidivittatus (Midge).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
 OC Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=7151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jaekle H., de Almeida J.C., Galler R., Kluding H., Lehrach H.,
 RA Edstroem J.E.;
 RT "Constant and variable parts in the balbiani ring 2 repeat unit and
 RT the translation termination region.";
 RL EMBO J. 1:883-888(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Edstroem J.E.;
 RL Submitted (NOV-1985) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X01863; CAA25984.1; -;
 FT NON TER 1
 FT NON TER 67
 SQ SEQUENCE 67 AA; 7430 MW; D507C0FE873984FC CRC64;

Query Match 100.0%; Score 25; DB 5; Length 67;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRP 4
 Db 51 GRRP 54

RESULT 18

Q64493 PRELIMINARY; PRT; 67 AA.
 AC Q64493;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Protein kinase (EC 2.7.1.37) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57/BL6; TISSUE=Kidney;
 RA Leitges M., Frokas T., Stabel S.;
 RT "Comparison of the mouse and rat protein kinase C gamma gene
 RT promoter.";
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X65720; CAA46636.1; -;
 DR HSP; P28867; 1PTQ.
 DR GO; GO:0004691; P:kinase activity; IEA.
 DR GO; GO:0016301; P:kinase activity; IEA.
 DR GO; GO:0004682; P:protein kinase CK2 activity; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR Pfam; PF00130; DAG_PE-bind.1.
 DR PRINTS; PRO0008; DAGPE0001.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
 KW Kinase; Transferase.
 FT NON TER 67
 SQ SEQUENCE 67 AA; 7335 MW; 266A16372A36A5F9 CRC64;

Query Match 100.0%; Score 25; DB 11; Length 67;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 14 GPRP 17

RESULT 19

Q23725 Q23725 PRELIMINARY; PRT; 69 AA.
AC Q23725;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gamma protein constant region (Fragment).
GN BRL.
OS Chironomus pallidivittatus (Midge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7151;
RN [1]
RP SEQUENCE FROM N.A.
RA Lendahl U., Saiga H., Hoeeg C., Edstroem J.E., Wieslander L.;
RT "Rapid and Concerted Evolution of Repeat Units in a Balbiani Ring
Gene.";
RL Genetics 117:43-49(1987).
DR EMBL; X06433; CAA29739.1; -.
FT NON_TER 1
FT NON_TER 69
SQ SEQUENCE 69 AA; 7218 MW; 16FA25C6A5644D48 CRC64;

Query Match 100.0%; Score 25; DB 5; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 5 GPRP 8

RESULT 20

Q8H408 Q8H408 PRELIMINARY; PRT; 69 AA.
AC Q8H408;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0492B07.18 protein.
GN P0492B07.18.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
clone:P0492E07.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004305; BAC20722.1; -.
SQ SEQUENCE 69 AA; 7836 MW; A7233809EB54E04B CRC64;

Query Match 100.0%; Score 25; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 14 GPRP 17

RESULT 21

Q9MAV4 Q9MAV4 PRELIMINARY; PRT; 70 AA.
AC Q9MAV4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F2401.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F2401 from chromosome
I.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]

Query Match 100.0%; Score 25; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 62 GPRP 65

RESULT 22

Q8TJ70 Q8TJ70 PRELIMINARY; PRT; 70 AA.
AC Q8TJ70;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Predicted protein.

GN MA3697.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., DeAtellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrelli A., Ye W., A.M.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettnier H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.,
 RA "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity."
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AEO11079; AAM07052.1; -.
 KW Complete proteome.
 SQ SEQUENCE 70 AA; 8271 MW; FB59PB85DBFEFA09 CRC64;
 Query Match 100.0%; Score 25; DB 17; Length 70;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 37 GPRP 40
 RESULT 23
 Q93M44
 ID Q93M44 PRELIMINARY; PRT; 71 AA.
 AC Q93M44;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative cytoplasmic membrane regulatory protein (fragment).
 GN HURR.
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UT25;
 RX MEDLINE=21311754; PubMed=11418569;
 RA Vanderpool C.K., Armstrong S.K.;
 RA "The Bordetella hhu Locus Is Required for Heme Iron Utilization."
 RL J. Bacteriol. 183:4278-4287(2001).
 DR EMBL; AY032627; AAK38152.1; -.
 DR InterPro; IPR006860; FecR.
 DR Pfam; PF04773; FecR; 1.
 FT NON TER 1 1
 SQ SEQUENCE 71 AA; 7975 MW; AA99D35076D30FA3 CRC64;
 Query Match 100.0%; Score 25; DB 2; Length 71;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 63 GPRP 66
 RESULT 24
 Q9XVW3
 ID Q9XVW3 PRELIMINARY; PRT; 72 AA.
 AC Q9XVW3;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE F41E7.8 protein.
 GN F41E7.8
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Lennard N.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99059613; PubMed=9851916;
 RA none;
 RA "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z68106; CAA92131.1; -.
 DR F41E7.8; T22081.
 DR WormPep; F41E7.8; CE19867.
 SQ SEQUENCE 72 AA; 7800 MW; 984037B62C980C1B CRC64;
 Query Match 100.0%; Score 25; DB 5; Length 72;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 41 GPRP 44
 RESULT 25
 Q80YF1
 ID Q80YF1 PRELIMINARY; PRT; 73 AA.
 AC Q80YF1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mixed-lineage kinase 3 (fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Kholodilov N.G., Rzhetskaya M., Burke R.E.;
 RT "Creation of cDNA probes for the Rat MLKs."
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY240868; AAO91627.1; -.
 DR GO; GO:0016301; F-kinase activity; IEA.
 KW Kinase.
 FT NON TER 1 1
 SQ SEQUENCE 73 AA; 7922 MW; 240540A12AA2B117 CRC64;
 Query Match 100.0%; Score 25; DB 11; Length 73;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 11 GPRP 14
 RESULT 26
 Q86984
 ID Q86984 PRELIMINARY; PRT; 73 AA.
 AC Q86984;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4516;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA de Bustos A., Loarce Y., Nicolas J.;
 RT "Phylogenetic analysis of genus Hordeum using ITS and chitinase gene
 sequences";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ400135; CAB77451.1; -
 FT NON_TER 1 1
 FT NON_TER 74 74
 SQ SEQUENCE 74 AA; 8020 MW; 0440BC46103B929B CRC64;
 Query Match 100.0%; Score 25; DB 10; Length 74;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 60 GPRP 63
 RESULT 29
 Q9P1C0 PRELIMINARY; PRT; 76 AA.
 ID Q9P1C0
 AC Q9P1C0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE PRO2900.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Cuyang S., Luo L., Bi J.,
 RA Liu M., He F.;
 RT "Functional prediction of the coding sequences of 121 new genes
 deduced by analysis of cDNA clones from human fetal liver.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF116718; AAF71138.1; -
 FT NON_TER 74 74
 SQ SEQUENCE 76 AA; 8424 MW; FBA4E9B5F2B2EC4 CRC64;
 Query Match 100.0%; Score 25; DB 4; Length 76;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 42 GPRP 45
 RESULT 30
 Q00397 PRELIMINARY; PRT; 76 AA.
 ID Q00397
 AC Q00397;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase isoform 2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Samuel S.J., Jung C.Y.;
 RT "Cloning of the promoter-proximal sequence of the 3-hydroxyacyl-CoA
 dehydrogenase gene.";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Orf2 (Fragment).
 CN ORF2.
 OS Galleria mellonella nuclear polyhedrosis virus (GmNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10447;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPONON=hitchhiker;
 RX MEDLINE=96187810; PubMed=8614994;
 RA Bauser C.A., Elick T.A., Praser M.J.;
 RT "Characterization of hitchhiker, a transposon insertion frequently
 associated with baculovirus FP mutants derived upon passage in the TN-
 368 cell line.";
 RT Virology 216:235-237(1996).
 DR EMBL; S81657; AAB36374.2; -
 FT NON_TER 1 1
 FT NON_TER 73 AA; 7979 MW; AFBDD75EA52E3ED1 CRC64;
 SQ SEQUENCE 73 AA; 7979 MW; AFBDD75EA52E3ED1 CRC64;
 Query Match 100.0%; Score 25; DB 12; Length 73;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 2 GPRP 5
 RESULT 27
 Q847P0 PRELIMINARY; PRT; 74 AA.
 ID Q847P0
 AC Q847P0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Yfcl protein (Fragment).
 OS Aster yellows phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Phycoplasmata.
 OX NCBI_TaxID=35779;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Melamed S., Tanne E., Ben-Haim R., Edelbaum O., Yogev D., Sela I.;
 RT "A Novel Approach to the Study of the Phytoplasmal Genome and the
 Characterization of Sixty Phytoplasmal Genes.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY191301; AAO61996.1; -
 FT NON_TER 74 74
 SQ SEQUENCE 74 AA; 8678 MW; DDB31EBC94F5B161 CRC64;
 Query Match 100.0%; Score 25; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 Db 9 GPRP 12
 RESULT 28
 Q9M3Q3 PRELIMINARY; PRT; 74 AA.
 ID Q9M3Q3
 AC Q9M3Q3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Chitinase (Fragment).
 GN CHI.
 OS Hordeum bulbosum (Bulbous barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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DR EMBL; AF001904; AAB58153.1; -.
FT NON TER 76
SQ SEQUENCE 76 AA; 7975 MW; C4E542EB19EDEFEE CRC64;

Query Match 100.0%; Score 25; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 29 GPRP 32

RESULT 31
Q9VF98 PRELIMINARY; PRT; 76 AA.
AC Q9VF98;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
DE C214865 protein.
GN C214865.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
RA George B.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Stadling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Rao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.N., Zhang M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003708; AAF55162.1; -.
DR FlyBase; FBgn0038314; CG14865.
SQ SEQUENCE 76 AA; 8950 MW; 40C6DB4C8BEC509D CRC64;

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Query Match 100.0%; Score 25; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 60 GPRP 63

RESULT 32
Q9NRK3 PRELIMINARY; PRT; 77 AA.
AC Q9NRK3;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE P8 protein.
GN P8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21226159; PubMed=1132721;
RA Lefranc D., Dubucquoi S., Almeras L., De Seze J., Tourvieille B.,
RA Dussart P., Aubert J.P., Vermeersch P., Prin L.,
RA "Molecular analysis of endogenous retrovirus HRSS-1: identification of
RT frameshift mutations in region encoding putative 28-kDa autoantigen.";
RL Biochem. Biophys. Res. Commun. 283:437-444 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX LeFranc D.,
RL Submitted (DDBJ-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216972; AAF76750.1; 42FF9090331FB92 CRC64;
SQ SEQUENCE 77 AA; 8223 MW; 42FF9090331FB92 CRC64;

Query Match 100.0%; Score 25; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 21 GPRP 24

RESULT 33
Q98A78 PRELIMINARY; PRT; 77 AA.
AC Q98A78;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Carbohydrate kinase.
GN MSF116.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003008; BAB52459.1; -.
DR HSSP; Q9TW2; ILII.

DR GO: GO:0016301; F:kinase activity; IEA.
 DR InterPro: IPR002173; PfKB.
 DR Pfam: PF00294; PfKB; 1.
 DR PROSITE: PS00584; PfKB KINASES_2; 1.
 DR KINASE: Complete proteome.
 SQ SEQUENCE 77 AA; 8223 MW; E8B5FA49ABCB9893 CRC64;
 Query Match 100.0%; Score 25; DB 16; Length 77;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 60 GPRP 63
 RESULT 34
 Q89YCI PRELIMINARY; PRT; 77 AA.
 AC Q89YCI;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Bsr0033 protein.
 GN BSR0033.
 OS Bradyrhizobium japonicum.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Bradyrhizobiaceae; Bradyrhizobium.
 CX NCBI_TaxID=375;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiyumi T.,
 RA Sasamoto S., Watanabe A., Ideawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005935; BAC45298.1; -;
 DR GO: GO:0016810; F:hydrolase activity, acting on carbon-nitrog. . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR002509; Polysacc deacet.
 DR Pfam: PF01522; Polysacc_deacet; 1.
 KW Complete proteome.
 SQ SEQUENCE 77 AA; 8587 MW; C970A6C191E96509 CRC64;
 Query Match 100.0%; Score 25; DB 16; Length 77;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 23 GPRP 26
 RESULT 35
 Q81MPO PRELIMINARY; PRT; 78 AA.
 AC Q81MPO;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN BA4207.
 OS Bacillus anthracis (strain Ames).
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=198094;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22608414; PubMed=12721629;
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,

RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
 RA Thomson B., Friedlander A.M., Koshler T.M., Hanna P.C., Kolsto A.-B.,
 RA Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 DR EMBL; AB017037; AAP27928.1; -;
 DR TIGR; BA4207; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 78 AA; 8536 MW; F4B455C107BF1C38 CRC64;
 Query Match 100.0%; Score 25; DB 16; Length 78;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 47 GPRP 50
 RESULT 36
 Q23726 PRELIMINARY; PRT; 79 AA.
 AC Q23726;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Gamma protein constant region (fragment).
 GN Brl.
 OS Chironomus pallidivittatus (Midge).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
 CC Chironomidae; Chironominae; Chironomus.
 CX NCBI_TaxID=7151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lendahl U., Saiga H., Hoeseg C., Edstroem J.E., Wieslander L.;
 RT "Rapid and Concerted Evolution of Repeat Units in a Balbiani Ring
 RT Gene";
 RL Genetics 117:43-49(1987).
 DR EMBL; X06434; CAA29740.1; -;
 DR PIR; S01718; S01718.
 FT NON TER 1 1
 FT NON TER 79 79
 SQ SEQUENCE 79 AA; 8305 MW; 74DA997F87BA2AAF CRC64;
 Query Match 100.0%; Score 25; DB 5; Length 79;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRP 4
 DB 7 GPRP 10
 RESULT 37
 O81534 PRELIMINARY; PRT; 80 AA.
 AC O81534;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Chalcone synthase (fragment).
 GN CHS.
 OS Saccharum officinarum (Sugarcane).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Saccharum.
 OX NCBI_TaxID=4547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Veronesi C., Thalouarn P.;
 RT "Sugarcane resistance to Striga hermonthica";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF079174; AAC27797.1; -.
 DR HSP; P30074; ID6F.
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0009058; P:biogenesis; IEA.
 DR InterPro; IPR001099; N-C synthase.
 DR Pfam; PF00195; Chal stil synt; 1.
 DR ProDom; PD000453; N-C synthase; 1.
 FT NON_TER 1
 FT NON_TER 80
 SQ SEQUENCE 80 AA; 8744 MW; 7B94776D2A46F418 CRC64;

Query Match 100.0%; Score 25; DB 10; Length 80;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 71 GPRP 74

RESULT 38

Q9NOUO Q9NOUO PRELIMINARY; PRT; 81 AA.
 AC Q9NOUO;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glucose transporter type four (Fragment).
 OS Bubalus bubalis (Domestic water buffalo).
 OC Sukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bubalus.
 OX NCBI_TaxID=89462;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patil S.S.B., Totey S.S.M.;
 RT "Partial cDNA sequence of Glucose transporter type four of Bubalus
 bubalis";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -/- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 DR EMBL; AF254423; AAF65841.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005351; F:sugar porter activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0008643; P:carbohydrate transport; IEA.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR001663; Sugar transpt.
 DR Pfam; PF00083; sugar tr; 1.
 DR PRINTS; PR00171; SUGRTRNSPORT.
 KW Sugar transporter; transmembrane; Transport.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 8700 MW; EBA42BEC3CB5EBB1 CRC64;

Query Match 100.0%; Score 25; DB 6; Length 81;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 46 GPRP 49

RESULT 39

Q81839 Q81839 PRELIMINARY; PRT; 83 AA.
 AC Q81839;

Q8QY94 Q8QY94 PRELIMINARY; PRT; 82 AA.
 AC Q8QY94;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORF2 (Fragment).
 OS TT virus.
 OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Heller F., Froesner G.G.;
 RT "Frequent multiple infection with different TT virus genotypes";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF464084; AAL78626.1; -.
 DR InterPro; IPR004118; TT ORF2.
 DR Pfam; PF02957; TT ORF2; 1.
 FT NON_TER 82
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8946 MW; 4BD430BED7862F56 CRC64;

Query Match 100.0%; Score 25; DB 12; Length 82;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 56 GPRP 59

RESULT 40

Q81845 Q81845 PRELIMINARY; PRT; 83 AA.
 AC Q81845;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hepatitis delta antigen (Fragment).
 GN HDAG.
 OS Hepatitis delta virus (HDV).
 OC Viruses; Deltavirus.
 OX NCBI_TaxID=12475;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Case J.L., Brown T.L., Colan E.J., Wignall F.S., Gerin J.L.;
 RT "A genotype of hepatitis D virus that occurs in northern South
 America";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:9016-9020(1993).
 DR EMBL; L22064; AAB02602.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR002506; HDV ag.
 DR Pfam; PF01517; HDV ag; 1.
 DR ProDom; PD002887; HDV ag; 1.
 FT NON_TER 1
 FT NON_TER 83
 SQ SEQUENCE 83 AA; 8968 MW; 3621E7DDE9C16920 CRC64;

Query Match 100.0%; Score 25; DB 12; Length 83;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 34 GPRP 37

RESULT 41

Q81839 Q81839 PRELIMINARY; PRT; 83 AA.
 AC Q81839;

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DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hepatitis delta antigen (Fragment).
GN HDAG
OS Hepatitis delta virus (HDV).
OC Viruses; Deltaviruses.
OC NCBI_TaxID=12475;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype III;
RX MEDLINE=9402306; PubMed=9415646;
RA Casey J.L., Brown T.L., Colan E.J., Wignall F.S., Gerin J.L.;
RT "A genotype of hepatitis B virus that occurs in northern South
RT America."
RL Proc. Natl. Acad. Sci. U.S.A. 90:9016-9020(1993).
RR EMBL; L22061; AB02598.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002506; HDV_ag.
DR Pfam; PF01517; HDV_ag; 1.
DR ProDom; PD002887; HDV_ag; 1.
FT NON TER
SQ SEQUENCE 83 AA; 8966 MW; 85E091599A4EB341 CRC64;

Query Match 100.0%; Score 25; DB 12; Length 83;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 34 GPRP 37

RESULT 42
Q8HYO0
ID Q8HYO0 PRELIMINARY; PRT; 84 AA.
AC Q8HYO0
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE Membrane cofactor protein (Fragment).
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OC NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22309086; PubMed=12421914;
RA Riley R.C., Tannenbaum P.L., Abbott D.H., Atkinson J.P.;
RT "Cutting Edge: Inhibiting Measles Virus Infection but Promoting
RT Reproduction: An Explanation for Splicing and Tissue-Specific
RT Expression of CD46."
RL J. Immunol. 169:5405-5409(2002).
DR EMBL; AY157982; AAN64664.1; -.
FT NON TER
SQ SEQUENCE 84 AA; 9279 MW; CC5BA7AC59AED187 CRC64;

Query Match 100.0%; Score 25; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 43
Q57593
ID Q57593 PRELIMINARY; PRT; 84 AA.
AC Q57593
DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE ORF V1.
OS Miscanthus streak virus.
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OC NCBI_TaxID=10825;
RN [1]
RP SEQUENCE FROM N.A.
RC Chatani M., Matsumoto Y., Mizuta H., Ikegami M., Boulton M.I.,
RA Davies J.W.;
RT "The nucleotide sequence and genome structure of Geminivirus
RT Miscanthus streak virus."
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; D01030; BAA00837.1; -.
DR FIR; JQ1356; JQ1356.
SQ SEQUENCE 84 AA; 8751 MW; A8CCDFB249776B1C CRC64;

Query Match 100.0%; Score 25; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 59 GPRP 62

RESULT 44
Q72913
ID Q72913 PRELIMINARY; PRT; 84 AA.
AC Q72913
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORF V1.
OS Miscanthus streak virus.
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OC NCBI_TaxID=10825;
RN [1]
RP SEQUENCE FROM N.A.
RC Sugimoto K., Hirochika H., Minobe Y., Kawamata H., Hibi T., Nanba S.,
RA Yamashita S., Iuchiaki T.;
RT "Nucleotide sequence of cloned Miscanthus streak virus DNA."
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; D00800; BAA25577.1; -.
SQ SEQUENCE 84 AA; 8721 MW; B57A04C249776B1C CRC64;

Query Match 100.0%; Score 25; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 59 GPRP 62

RESULT 45
Q98AH9
ID Q98AH9 PRELIMINARY; PRT; 86 AA.
AC Q98AH9
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Transposase.
GN MGR5992.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OC NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

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RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Kakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT *Mesorhizobium loti*,"
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003008; BAB52351.1; -;
DR InterPro: IPR001207; Transposase_mutatr.
DR Pfam: PF00872; Transpos_mutator; 1.
KW Complete proteome.
SQ SEQUENCE 86 AA; 9753 MW; 3A1DFC5DAD1763D1 CRC64;

Query Match 100.0%; Score 25; DB 16; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 75 GPRP 78

RESULT 46

Q9ADA9 ID Q9ADA9 PRELIMINARY; PRT; 86 AA.
AC Q9ADA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SC0518 (Fragment).
GN SC0518 OR SCF6.14.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Randeram M.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaire D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome,"
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Randeram M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders A., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietersreik A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL939105; CAB58278.2; -;
DR GO: GO:000325; C:nitrate reductase complex; IEA.
DR GO: GO:0008940; F:nitrate reductase activity; IEA.

DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR003816; Nitrate_red_gam.
DR Pfam: PF02665; Nitrate_red_gam; 1.
KW Hypothetical protein; Complete proteome.
FT NON TER 86
SQ SEQUENCE 86 AA; 9502 MW; 7A9PBCF466863A1C CRC64;

Query Match 100.0%; Score 25; DB 16; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 28 GPRP 31

RESULT 47

Q845Q9 ID Q845Q9 PRELIMINARY; PRT; 87 AA.
AC Q845Q9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Relaxase/helicase (Fragment).
GN TCCA.
OS Aeromonas salmonicida.
OC Plasmid pRASI.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2402-89;
RA Sorum H., L'Abée-Lund T.M., Solberg A., Wold A.;
RT "The integron containing IncU R plasmids pRASI and pAR-32 from the
RT fish pathogen Aeromonas salmonicida,"
RL Antimicrob. Agents Chemother. 47:1285-1290(2003).
DR EMBL: AJ517790; CAD57190.1; -;
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
DR GO: GO:0004386; F:helicase activity; IEA.
KW Helicase; Plasmid.
FT NON TER 1
SQ SEQUENCE 87 AA; 9759 MW; 50EA3AC58103D1A2 CRC64;

Query Match 100.0%; Score 25; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 14 GPRP 17

RESULT 48

P87913 ID P87913 PRELIMINARY; PRT; 87 AA.
AC P87913;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ICPOC.
GN ALPHA 0.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F;
RA Carter K.L., Roizman B.;
RT "Alternatively spliced mRNAs predicted to yield frame-shift genes and
RT stable intron 1 RNAs of the herpes simplex virus 1 regulatory gene
RT alpha 0 accumulate in the cytoplasm of infected cells,"

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RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1996).
DR EMBL: U70039; AA837296.1; -.
SQ SEQUENCE 87 AA; 9466 MW; DDB3024B5D178483 CRC64;

Query Match
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 34 GPRP 37

RESULT 49
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ID O39500 PRELIMINARY; PRT; 87 AA.
AC O39500;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UL0.5 protein.
GN UL0.5
OS Bovine herpesvirus type 1 (strain Jura).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jura;
EX MEDLINE=92219360; PubMed=1313901;
RA With U.V., Fraefel C., Vost B., Vlcek C., Paces V., Schwytzer M.;
RT "Immediate early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are
RT 3' coterminal and encode a putative zinc finger transactivator
RT protein.";
RL J. Virol. 66:2763-2772(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Jura;
EX Schwytzer M., Paces V., Letchworth G.J., Misra V., Buik H.J.,
RA Lowery D.B., Simard C., Bello L.J., Thiry E., Vlcek C.;
RT "Complete DNA sequence of bovine herpesvirus 1.";
RL Submitted (SRP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ004801; CAA06136.1; -.
SQ SEQUENCE 87 AA; 9550 MW; 9703325A10D22897 CRC64;

Query Match
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 50
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AC O9CBF6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein ML2035.
GN ML2035
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
EX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

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RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrall B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL: AL583924; CAC30990.1; -.
DR PIR: F87163; F87163.
DR Leproma; ML2035; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 87 AA; 9917 MW; 90697B6FD9BADBEB CRC64;

Query Match
Best Local Similarity 100.0%; Score 25; DB 16; Length 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 24 GPRP 27

Search completed: September 7, 2004, 19:00:49
Job time : 119 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein ~ protein search, using sw model

Run on: September 7, 2004, 19:23:32 ; Search time 405 Seconds
(without alignments)

9.640 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 53782

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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; Sequence 1, Application PC/TUS0307665

ALIGNMENTS

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4	25	100.0	4	1	PCT-US98-27060-6
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6	25	100.0	4	3	US-07-705-071-5
7	25	100.0	4	5	US-08-138-820-4
8	25	100.0	4	6	US-08-260-514-4
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; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; APPLICANT: BRESAGEN LIMITED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRIMATE NEURAL CELL
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 18465-0023
; CURRENT APPLICATION NUMBER: PCT/US03/07665
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: 60/364,381
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US03-07665-1

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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GPRP 4

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RESULT 2
PCT-US03-24864-1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; APPLICANT: BRESAGEN, LTD.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL DIFFERENTIATION
; TITLE OF INVENTION: OF EMBRYONIC STEM CELLS
; FILE REFERENCE: 18465-0024
; CURRENT APPLICATION NUMBER: PCT/US03/24864
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/401,968
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US 60/459,090
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US03-24864-1

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Query Match      100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: BRESAGEN, LTD.
; APPLICANT: MEDICAL COLLEGE OF GEORGIA RESEARCH INSTITUTE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENRICHMENT OF NEURAL STEM
; TITLE OF INVENTION: CELLS USING CERAMIDE ANALOGS

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; FILE REFERENCE: 18377-0024
; CURRENT APPLICATION NUMBER: PCT/US03/30112
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 60/413,510
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/485,351
; PRIOR FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 16
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; LENGTH: 4
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US03-30112-1

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RESULT 4
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; GENERAL INFORMATION:
; SEQUENCE 6, Application PC/TUS9827060
; APPLICANT: IMARX PHARMACEUTICAL CORP.
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR-1536
; CURRENT APPLICATION NUMBER: PCT/US98/27060
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: 08/993,165
; EARLIER FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: novel sequence
PCT-US98-27060-6

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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
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Qy      1 GPRP 4
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Db      1 GPRP 4

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RESULT 5
PCT-US98-27060-6
; SEQUENCE 6, Application PC/TUS9827060A
; GENERAL INFORMATION:
; APPLICANT: IMARX PHARMACEUTICAL
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1536
; CURRENT APPLICATION NUMBER: PCT/US98/27060A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US98-27060-6

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
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Db 1 GPRP 4

RESULT 6

US-07-705-071-5
Sequence 5, Application US/07705071
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07705,071
FILING DATE: 19910524
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-07-705-071-5

Query Match 100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GPRP 4

RESULT 7

US-08-138-820-4
Sequence 4, Application US/08138820
GENERAL INFORMATION:
APPLICANT: Klein, Scott I.
APPLICANT: Molino, Bruce F.
TITLE OF INVENTION: ANTI-THROMBOTIC AZACYCLOALKYLALKANOYL
TITLE OF INVENTION: PEPTIDES AND PSEUDOPETIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43

CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08138,820
FILING DATE: 15-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Darkes, Paul R.
REGISTRATION NUMBER: 33,862
REFERENCE/DOCKET NUMBER: A1158
TELEPHONE: (215) 454-3820
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-138-820-4
Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|
|
|
|
Db 1 GPRP 4

RESULT 8

US-08-260-514-4
Sequence 4, Application US/08260514
GENERAL INFORMATION:
APPLICANT: Muir, Thomas W.
APPLICANT: Williams, Michael J.
APPLICANT: Ginsberg, Mark H.
APPLICANT: Kent, Stephen B. H.
APPLICANT: Chen, Yi-Ping
APPLICANT: O'Toole, Timothy E.
TITLE OF INVENTION: Structural Models for Cytoplasmic
TITLE OF INVENTION: Domains of Transmembrane Receptors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,514
FILING DATE: 15-JUN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 30457.6-US-01
TELEPHONE: (310) 445-1140
TELEFAX: (310) 445-9031

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: internal
 ORGANISM: *Ligand sequence recognized by integrin*

US-08-260-514-4
 Query Match 100.0%; Score 25; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 9
 US-08-753-781B-2
 ; Sequence 2, Application US/08753781B
 ; GENERAL INFORMATION:
 ; APPLICANT: Markland, Francis S
 ; APPLICANT: Bush, Larry R
 ; APPLICANT: Swenson, Stephen
 ; APPLICANT: Sanchez, Eladio F
 ; TITLE OF INVENTION: Thrombolytic Agents with Antithrombotic
 ; TITLE OF INVENTION: Properties
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/753,781B
 FILING DATE: 02-DEC-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Noonan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 96,2056
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312 913 0001
 TELEFAX: 312 913 0002
 TELEX:

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-753-781B-2
 Query Match 100.0%; Score 25; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 10
 US-08-982-981-1
 ; Sequence 1, Application US/08982981
 ; GENERAL INFORMATION:
 ; APPLICANT: Markland Jr., Francis S.
 ; APPLICANT: Bush, Larry R.
 ; APPLICANT: Swenson, Stephen
 ; APPLICANT: Flores Sanchez, Eladio
 ; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
 ; TITLE OF INVENTION: ACTIVITY
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Diatide, Inc.
 ; STREET: 9 Delta Drive
 ; CITY: Londonderry
 ; STATE: NH
 ; COUNTRY: USA
 ; ZIP: 03053
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/982,981
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/753,781
 ; FILING DATE: 02-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McDaniels, Patricia A.
 ; REGISTRATION NUMBER: 33,194
 ; REFERENCE/DOCKET NUMBER: DITI 124.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 603 437 8970
 ; TELEFAX: 603 437 8977
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-982-981-1

Query Match 100.0%; Score 25; DB 13; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 ||||
 Db 1 GPRP 4

RESULT 11
 US-09-040-712-3
 ; Sequence 3, Application US/09040712
 ; GENERAL INFORMATION:
 ; APPLICANT: Durbin, Dennis A.
 ; APPLICANT: Lee, Theodore T.
 ; APPLICANT: Ratnikov, Boris I.
 ; APPLICANT: Hillman, Robert S.
 ; APPLICANT: Smith, Jeffrey W.
 ; TITLE OF INVENTION: AGGLUTININ ASSAYS IN BLOOD
 ; FILE REFERENCE: 22608-0014P1
 ; CURRENT APPLICATION NUMBER: US/09/040,712
 ; CURRENT FILING DATE: 1998-03-18
 ; PRIOR APPLICATION NUMBER: US 08/820,999
 ; PRIOR FILING DATE: 1997-03-20
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 3

```
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(4)
/ OTHER INFORMATION: Peptide inhibitor of fibrin polymerization.
US-09-040-712-3

Query Match          100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 12
US-09-091-578B-5
; Sequence 5, Application US/09091578B
; GENERAL INFORMATION:
; APPLICANT: MADISON, EDWIN L.
; TITLE OF INVENTION: TARGETED THERAPEUTIC OR DIAGNOSTIC
; FILE REFERENCE: 19191.0002
; CURRENT APPLICATION NUMBER: US/09/091.578B
; CURRENT FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PCT/US96/20577
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 60/009,028
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: artificial construct
US-09-091-578B-5

Query Match          100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 13
US-09-218-660-4
; Sequence 4, Application US/09218660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Shen, Dekang
; APPLICANT: Wu, Guanli
; TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And
; TITLE OF INVENTION: Therapeutic Use
; FILE REFERENCE: DUP-0307
; CURRENT APPLICATION NUMBER: US/09/218,660
; CURRENT FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 08/660,032
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 08/640,464
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/497,684
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 22

Query Match          100.0%; Score 25; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 14
US-09-376-529-2
; Sequence 2, Application US/09376529
; GENERAL INFORMATION:
; APPLICANT: Thakur, Madhukar L.
; TITLE OF INVENTION: Imaging With TC-99 Labeled
; FILE REFERENCE: THA01.NP003
; CURRENT APPLICATION NUMBER: US/09/376,529
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/096,803
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown
US-09-376-529-2

Query Match          100.0%; Score 25; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 15
US-09-593-117-6
; Sequence 6, Application US/09593117
; GENERAL INFORMATION:
; APPLICANT: Evan C., Unger
; APPLICANT: Wu, Yundiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1594
; CURRENT APPLICATION NUMBER: US/09/593,117
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 08/993,165
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-593-117-6

Query Match          100.0%; Score 25; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-218-660-4
```

```
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
    ||||
Db 1 GPRP 4

RESULT 16
US-09-639-634A-4
; Sequence 4, Application US/09639634A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Chrzan, Zofia J
; APPLICANT: Mancel, James J
; APPLICANT: Toledo-Valasquez, David
; APPLICANT: Windisch, Vincent
; APPLICANT: Woodward, Rick G.
; APPLICANT: Salazar, Diane (Deceased) C
; APPLICANT: Salazar, Richard (Legal Representative) C
; APPLICANT: Vemuri, Narasimha M
; APPLICANT: Gardetto, Anthony J.
; APPLICANT: Matthew, Powers R.
; APPLICANT: Kubiak, Gregory G.
; APPLICANT: Liu, Robert C.
; APPLICANT: Vanasse, Benoit J.
; APPLICANT: Sherbine, James P.
; APPLICANT: Rodriguez, Walter
; APPLICANT: Sledzski, Adam W.
; TITLE OF INVENTION: STABLE NON-HYDROSCOPIC CRYSTALLINE FORM OF N-[N-(4-(PIPERIDIN-1-YL)BUTANOYL)-N-ETHYLGLYCYL]ASPARTYL-L-BETA-CYCLOHEXYL ALANINE A
; TITLE OF INVENTION: INTERMEDIATES THEREOF, AND PREPARATION THEREOF AND OF ANTITHROMB
; TITLE OF INVENTION: AZACYCLOALKYALKANOYL PEPTIDES AND PSEUDOPEPTIDES
; FILE REFERENCE: A2234B US
; CURRENT APPLICATION NUMBER: US/09/639,634A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 09/251,030
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: PCT/US97/14756
; PRIOR FILING DATE: 1997-08-21
; PRIOR APPLICATION NUMBER: 60/024,284
; PRIOR FILING DATE: 1996-08-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide capable of inhibiting binding of fibrinogen to platelets
US-09-639-634A-4

Query Match 100.0%; Score 25; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
    ||||
Db 1 GPRP 4

RESULT 17
US-09-687-156A-1
; Sequence 1, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Messmer, David S
; APPLICANT: Thaler, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-1

Query Match 100.0%; Score 25; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
    ||||
Db 1 GPRP 4

RESULT 18
US-09-699-679A-4
; Sequence 4, Application US/09699679A
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, Dekang
; APPLICANT: Wu, Guanli
; TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And Therapeutic Use
; FILE REFERENCE: UNGR1598
; CURRENT APPLICATION NUMBER: US/09/699,679A
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/218,660
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 08/660,032
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 08/640,464
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/497,684
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-699-679A-4

Query Match 100.0%; Score 25; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
    ||||
Db 1 GPRP 4

RESULT 19
US-09-763-777B-2
; Sequence 2, Application US/09763777B
; GENERAL INFORMATION:
; APPLICANT: Thakur, Madhukar (Matthew) L.
; TITLE OF INVENTION: Imaging with TC-99m Labeled Fibrin Alpha Chain Peptide
; FILE REFERENCE: 8321-119
; CURRENT APPLICATION NUMBER: US/09/763,777B
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/19011
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,803
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
```

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of N-terminus tripeptide identified in SEQ
; OTHER INFORMATION: ID NO: 1
US-09-763-777B-2

Query Match      100.0%; Score 25; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 20
US-09-779-054-16
; Sequence 16, Application US/09779054
; GENERAL INFORMATION:
; APPLICANT: Lu, Xinxie
; APPLICANT: Kakkar, Vijay
; TITLE OF INVENTION: USE OF DENDROASPIN AS A SCAFFOLD FOR NON-DENDROASPIN DOMAINS
; FILE REFERENCE: A-70312/TAL/ANS
; CURRENT APPLICATION NUMBER: US/09/779,054
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: GB 0002625.2
; PRIOR FILING DATE: 2000-02-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: thrombin-binding sequence
US-09-779-054-16

Query Match      100.0%; Score 25; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 21
US-09-813-484-6
; Sequence 6, Application US/09813484
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Precur
; FILE REFERENCE: UNGR1600
; CURRENT APPLICATION NUMBER: US/09/813,484
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/929,847
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-09-813-484-6

Query Match      100.0%; Score 25; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 22
US-09-931-009A-2
; Sequence 2, Application US/09931009A
; GENERAL INFORMATION:
; APPLICANT: Smith, Theresa H.
; TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
; FILE REFERENCE: US 1257/01 (VA)
; CURRENT APPLICATION NUMBER: US/09/931,009A
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown. Obtained from a commercial source.
US-09-931-009A-2

Query Match      100.0%; Score 25; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 23
US-10-016-569A-25
; Sequence 25, Application US/10016569A
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kua-Shiyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: PL379
; CURRENT APPLICATION NUMBER: US/10/016,569A
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
US-10-016-569A-25

Query Match      100.0%; Score 25; DB 26; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 24
US-10-046-801-6
; Sequence 6, Application US/10046801
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
```

```
/ CURRENT FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: US/09/540,448
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 08/925,353
/ PRIOR FILING DATE: 1997-09-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-10-046-801-6

Query Match          100.0%; Score 25; DB 26; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 25
US-10-308-644-25
; Sequence 25, Application US/10308644
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: FI379
; CURRENT APPLICATION NUMBER: US/10/308,644
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
US-10-308-644-25

Query Match          100.0%; Score 25; DB 29; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 26
US-10-674-756-9
; Sequence 9, Application US/10674756
; GENERAL INFORMATION:
; APPLICANT: FORWOOD, JADE KENNETH
; APPLICANT: MORRIS, MICHAEL BRADLEY
; TITLE OF INVENTION: RECEPTOR EXPRESSED IN PLURIPOTENT CELLS
; FILE REFERENCE: 18377-0025
; CURRENT APPLICATION NUMBER: US/10/674,756
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: AU 2002952398
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-10-674-756-9

Query Match          100.0%; Score 25; DB 31; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 27
PCT-US02-29060-101
; Sequence 101, Application PC/TUS0229060
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Smith, Jeffrey W.
; APPLICANT: Chen, Emily I.
; APPLICANT: Kridel, Steven J.
; TITLE OF INVENTION: Selective Substrates for Matrix
; TITLE OF INVENTION: Metalloproteinases
; FILE REFERENCE: FP-LJ 5413
; CURRENT APPLICATION NUMBER: PCT/US02/29060
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/953,592
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
PCT-US02-29060-101

Query Match          76.0%; Score 19; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
Db 1 PRP 3

RESULT 28
US-09-953-592-101
; Sequence 101, Application US/09953592
; GENERAL INFORMATION:
; APPLICANT: Smith, Jeffrey W.
; APPLICANT: Chen, Emily I.
; APPLICANT: Kridel, Steven J.
; TITLE OF INVENTION: Selective Substrates for Matrix
; TITLE OF INVENTION: Metalloproteinases
; FILE REFERENCE: P-LJ 4851
; CURRENT APPLICATION NUMBER: US/09/953,592
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-953-592-101

Query Match          76.0%; Score 19; DB 25; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

US-07-884-495-2
; Sequence 2, Application US/07884495
; GENERAL INFORMATION:
; APPLICANT: Tan, Paris Som Tjwan
; APPLICANT: Konings, Wilhelmus Nicolaas
; TITLE OF INVENTION: PROTEIN FROM LACTIC ACID BACTERIA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/884,495
; FILING DATE: 19920515
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91201185.5
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, Thomas F
; REGISTRATION NUMBER: 16,579
; REFERENCE/DOCKET NUMBER: 2805/41484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-884-495-2
Query Match 76.0%; Score 19; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPAP 4
RESULT 32
US-09-868-677-13
; Sequence 13, Application US/09868677
; GENERAL INFORMATION:
; APPLICANT: Samuel Davis, Nicholas W. Gale, George D. Vancopoulos, and
; APPLICANT: Neil Stahl
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL ACTIVITY OF LIGANDS
; FILE REFERENCE: REG 670-A-US
; CURRENT APPLICATION NUMBER: US/09/868,677
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US99/30900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,387
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-868-677-13

Qy 2 PRP 4
Db 1 PRP 3
RESULT 29
US-10-243-613-101
; Sequence 101, Application US/10243613
; GENERAL INFORMATION:
; APPLICANT: Smith, Jeffrey W.
; APPLICANT: Chen, Emily I.
; APPLICANT: Kridel, Steven J.
; TITLE OF INVENTION: Selective Substrates for Matrix
; TITLE OF INVENTION: Metalloproteinases
; FILE REFERENCE: P-LJ 5432
; CURRENT APPLICATION NUMBER: US/10/243,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/953,592
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 3
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-243-613-101
Query Match 76.0%; Score 19; DB 28; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PRP 4
Db 1 PRP 3
RESULT 30
PCT-US02-24572-115
; Sequence 115, Application PC/TUS0224572
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; TITLE OF INVENTION: Positional Biosensors for the Assay of Cellular Biochemistry
; FILE REFERENCE: 01-1022-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/24572
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
PCT-US02-24572-115
Query Match 76.0%; Score 19; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PRP 4
Db 2 PRP 4
RESULT 31

Query Match 76.0%; Score 19; DB 23; Length 4;
 Best Local Similarity 75.0%; Pred. No. 5.5e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
 |||
 Db 1 GPRP 4

RESULT 33
 US-10-211-088-115
 ; Sequence 115, Application US/10211088
 ; GENERAL INFORMATION:
 ; APPLICANT: Bright, Gary R. David
 ; APPLICANT: Premkumar, D. David
 ; APPLICANT: Chen, Yih-Tai
 ; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
 ; FILE REFERENCE: 01-1022-US
 ; CURRENT APPLICATION NUMBER: US/10/211,088
 ; PRIOR FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: 60/309,395
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/341,589
 ; PRIOR FILING DATE: 2001-12-13
 ; NUMBER OF SEQ ID NOS: 366
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 115
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Binding domain

US-10-211-088-115

Query Match 76.0%; Score 19; DB 28; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
 |||
 Db 2 PRP 4

RESULT 34
 US-10-275-427A-34
 ; Sequence 34, Application US/10275427A
 ; GENERAL INFORMATION:
 ; APPLICANT: Nash et al.
 ; TITLE OF INVENTION: Molecules that Modulate Ubiquitin-Dependent Proteolysis and
 ; FILE REFERENCE: MTSI-P01-011
 ; CURRENT APPLICATION NUMBER: US/10/275,427A
 ; CURRENT FILING DATE: 2002-11-04
 ; PRIOR APPLICATION NUMBER: PCT/CA01/00632
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 34
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: CDP Peptide
 ; NAME/KEY: MOD_RES
 ; LOCATION: (4)..(4)
 ; OTHER INFORMATION: PHOSPHORYLATION

US-10-275-427A-34

Query Match 76.0%; Score 19; DB 28; Length 4;
 Best Local Similarity 75.0%; Pred. No. 5.5e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
 |||
 Db 1 GPRP 4

RESULT 35
 PCT-US02-30533-331
 ; Sequence 331, Application PC/TUS0230533
 ; GENERAL INFORMATION:
 ; APPLICANT: Cowley, Michael
 ; APPLICANT: Cone, Roger
 ; APPLICANT: Low, Malcolm
 ; APPLICANT: Butler, Andrew
 ; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Screen for Agents
 ; FILE REFERENCE: 0899-63986
 ; CURRENT APPLICATION NUMBER: PCT/US02/30533
 ; PRIOR FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: 60/324,406
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 60/392,109
 ; PRIOR FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 352
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 331
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Polypeptide variation

PCT-US02-30533-331

Query Match 72.0%; Score 18; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
 |||
 Db 1 GPR 3

RESULT 36
 PCT-US02-30533A-331
 ; Sequence 331, Application PC/TUS0230533A
 ; GENERAL INFORMATION:
 ; APPLICANT: Cowley, Michael
 ; APPLICANT: Cone, Roger
 ; APPLICANT: Low, Malcolm
 ; APPLICANT: Butler, Andrew
 ; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Beh
 ; FILE REFERENCE: 899-63986
 ; CURRENT APPLICATION NUMBER: PCT/US02/30533A
 ; CURRENT FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: US 60/324,406
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: US 60/392,109
 ; PRIOR FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 352
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 331
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Polypeptide variation

PCT-US02-30533A-331

Query Match 72.0%; Score 18; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
 |||

Db 1 GPR 3

RESULT 37

PCT-US02-31944A-331
; Sequence 331, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Gbatei, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 331
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide variation
PCT-US02-31944A-331

Query Match 72.0%; Score 18; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3

Db 1 GPR 3

RESULT 38

US-09-376-529-1
; Sequence 1, Application US/09376529
; GENERAL INFORMATION:
; APPLICANT: Thakur, Madhukar L.
; TITLE OF INVENTION: Imaging With TC-99 Labeled
; TITLE OF INVENTION: Fibrin-Alpha-Chain Peptide
; FILE REFERENCE: THA01.NP003
; CURRENT APPLICATION NUMBER: US/09/376,529
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/096,803
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 4.0
; SEQ ID NO 1
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown
US-09-376-529-1

Query Match 72.0%; Score 18; DB 17; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3

|||

Db 1 GPR 3

RESULT 39

US-09-623-548A-1153
; Sequence 1153, Application US/09623548A
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1153
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1153

Query Match 72.0%; Score 18; DB 20; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3

Db 1 GPR 3

RESULT 40

US-09-657-276-1153
; Sequence 1153, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1153
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-657-276-1153.

Query Match 72.0%; Score 18; DB 20; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 1 GPR 3

RESULT 41
US-09-763-777B-1
; Sequence 1, Application US/09763777B
; GENERAL INFORMATION:
; APPLICANT: Thakur, Madhukar (Matthew) L.
; TITLE OF INVENTION: Imaging with TC-99m Labeled Fibrin Alpha
; TITLE OF INVENTION: Chain Peptide
; FILE REFERENCE: 8321-119
; CURRENT APPLICATION NUMBER: US/09/763,777B
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/19011
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,803
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminus tripeptide portion of
; OTHER INFORMATION: fibrin-alpha-chain peptide
US-09-763-777B-1

Query Match 72.0%; Score 18; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 1 GPR 3

RESULT 42
PCT-US03-08732-1
; Sequence 1, Application PC/TUS0308732
; GENERAL INFORMATION:
; APPLICANT: Wescott, Charles R.
; APPLICANT: Sato, Aaron K.
; TITLE OF INVENTION: FIBRINOGEN BINDING MOIETIES
; FILE REFERENCE: DYX-036.1 PCT; DYX-036.1 US
; CURRENT APPLICATION NUMBER: PCT/US03/08732
; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/367,645
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: N-terminal peptide of fibrinogen alpha chain
PCT-US03-08732-1

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 1 GPR 3

RESULT 43
PCT-US03-16468A-13
; Sequence 13, Application PC/TUS0316468A
; GENERAL INFORMATION:
; APPLICANT: Restoragen Inc.
; APPLICANT: Seo, Jin Seog
; APPLICANT: Strydom, Daniel
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: Polypeptide Cleavage Process
; FILE REFERENCE: 1627.026WO1
; CURRENT APPLICATION NUMBER: PCT/US03/16468A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,488
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Construct
PCT-US03-16468A-13

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 2 GPR 4

RESULT 44
PCT-US03-16648A-39
; Sequence 39, Application PC/TUS0316648A
; GENERAL INFORMATION:
; APPLICANT: Restoragen Inc.
; APPLICANT: Holmquist, Barton
; APPLICANT: Strydom, Daniel
; APPLICANT: Gensalk, X.
; APPLICANT: Cryer, R.
; TITLE OF INVENTION: Peptide Amidation Process
; FILE REFERENCE: 1627.012WO1
; CURRENT APPLICATION NUMBER: PCT/US03/16648A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,362
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
PCT-US03-16648A-39

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 2 GPR 4

RESULT 45
PCT-US97-12974A-35
; Sequence 35, Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: 23 Jul 97
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/685,589
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 35:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-35
Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 GPR 3
Db 1 GPR 3
RESULT 46
PCT-US97-12974A-36
; Sequence 36, Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: 23 Jul 97
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/685,589
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 35:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-35
Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 GPR 3
Db 1 GPR 3
RESULT 47
PCT-US97-12974A-37
; Sequence 37, Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12974A
FILING DATE: 23 Jul 97
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/685,589
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 36:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-36
Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 GPR 3
Db 1 GPR 3
RESULT 47
PCT-US97-12974A-37
; Sequence 37, Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 8067-048-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-35

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GPR 3
Db 1 GPR 3

RESULT 48
PCT-US97-19557-36
Sequence 36, Application PC/TUS9719557
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19557
FILING DATE: herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-048-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-36

Query Match 72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GPR 3
Db 1 GPR 3

RESULT 49
US-08-037-621-4
Sequence 4, Application US/08037621
GENERAL INFORMATION:
APPLICANT: Robert F. Hird, Edward F. Cosgrove
TITLE OF INVENTION: Test Kits and Methods for Rapidly
TITLE OF INVENTION: Testing for Contamination By Microorganisms.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hird and Cosgrove
STREET: 1110 Burnett Avenue, Suite D
CITY: Concord
STATE: California
COUNTRY: USA
ZIP: 94520
COMPUTER READABLE FORM:
MEDIUM TYPE: MD2-HD, DS/HD, 1.2 MB
COMPUTER: Memorex Telex
OPERATING SYSTEM: MS-DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,621
FILING DATE: 25-March, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA: None
ATTORNEY/AGENT INFORMATION:
NAME: Applicants
REGISTRATION NUMBER: Not Applicable
REFERENCE/DOCKET NUMBER: 15612-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 676-2733
TELEFAX: (510) 676-2734
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 Amino Acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1-4
IDENTIFICATION METHOD: Similarity to other signal
IDENTIFICATION METHOD: sequences, hydrophobic
OTHER INFORMATION: xaa in location 1 of following
OTHER INFORMATION: sequence is Tosyl
US-08-037-621-4

Query Match 72.0%; Score 18; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GPR 3
Db 2 GPR 4

RESULT 50
US-08-263-758-28
Sequence 28, Application US/08263758
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 37

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Allegretti & Witcoff, Ltd.
;; STREET: 10 South Wacker Drive Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/263,758
;; FILING DATE: 22-JUN-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/653,012
;; FILING DATE: 08-FEB-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDonnell, John J
;; REGISTRATION NUMBER: 26,949
;; REFERENCE/DOCKET NUMBER: 90,1104
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312 715 1000
;; TELEFAX: 312 715 1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-263-758-28

Query Match 72.0%; Score 18; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
|||
Db 1 GPR 3

Search completed: September 7, 2004, 19:32:29
Job time : 406 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:24:42 ; Search time 59 Seconds

(without alignments)
8.769 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 702585 seqs, 129335945 residues

Total number of hits satisfying chosen parameters: 6105

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

Pending Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	4	1	PCT-US04-10121-1
2	25	100.0	4	1	PCT-US04-16828-4
3	25	100.0	4	1	PCT-US03-40762-1
4	18	72.0	3	6	US-10-489-804-331
5	18	72.0	3	6	US-10-477-712B-62
6	18	72.0	3	6	US-10-459-030B-2
7	18	72.0	3	6	US-10-651-584C-90
8	18	72.0	4	5	US-09-804-733B-24
9	18	72.0	4	6	US-10-459-030B-4
10	18	72.0	4	6	US-10-821-240A-151
11	18	72.0	4	6	US-10-720-831-5
12	17	68.0	4	7	US-60-548-401-3581
13	16	64.0	4	1	PCT-US04-10121-4
14	16	64.0	4	1	PCT-US03-40762-4
15	15	60.0	4	6	US-10-686-884-9
16	14	56.0	3	7	US-60-548-401-486
17	14	56.0	4	1	PCT-US04-04137-36
18	14	56.0	4	1	PCT-US04-11167-158
19	14	56.0	4	5	US-09-852-910B-158
20	14	56.0	4	6	US-10-778-253-36
21	14	56.0	4	7	US-60-548-401-518
22	14	56.0	4	7	US-60-548-401-519
23	13	52.0	2	7	US-60-548-401-3546
24	13	52.0	2	7	US-60-548-401-3550
25	13	52.0	3	1	PCT-US04-02004-70
26	13	52.0	3	1	PCT-US03-33658A-26

27	13	52.0	3	6	US-10-682-011-16	Sequence 16, Appl
28	13	52.0	3	7	US-60-548-401-3561	Sequence 3561, Ap
29	13	52.0	3	7	US-60-548-401-3562	Sequence 3562, Ap
30	13	52.0	3	7	US-60-548-401-3565	Sequence 3565, Ap
31	13	52.0	3	7	US-60-548-401-3566	Sequence 3566, Ap
32	13	52.0	4	1	PCT-US03-35026-224	Sequence 224, App
33	13	52.0	4	1	PCT-US04-04137-26	Sequence 26, Appl
34	13	52.0	4	1	PCT-US04-04137-28	Sequence 28, Appl
35	13	52.0	4	1	PCT-US03-41269-81	Sequence 81, Appl
36	13	52.0	4	1	PCT-US04-11167-171	Sequence 171, Appl
37	13	52.0	4	1	PCT-US03-41261-81	Sequence 81, Appl
38	13	52.0	4	1	PCT-US03-41335-26	Sequence 26, Appl
39	13	52.0	4	1	PCT-US04-10121-2	Sequence 2, Appl
40	13	52.0	4	1	PCT-US03-40762-2	Sequence 2, Appl
41	13	52.0	4	5	US-09-852-910B-171	Sequence 171, Appl
42	13	52.0	4	5	US-09-421-545-2	Sequence 1, Appl
43	13	52.0	4	5	US-09-421-545-2	Sequence 1, Appl
44	13	52.0	4	5	US-09-558-973-1	Sequence 1, Appl
45	13	52.0	4	5	US-09-558-973-2	Sequence 2, Appl
46	13	52.0	4	5	US-09-423-578A-18	Sequence 18, Appl
47	13	52.0	4	5	US-09-310-685-23	Sequence 23, Appl
48	13	52.0	4	5	US-09-695-807-1	Sequence 1, Appl
49	13	52.0	4	5	US-09-695-807-2	Sequence 2, Appl
50	13	52.0	4	5	US-09-593-695D-48	Sequence 48, Appl
51	13	52.0	4	5	US-09-825-423C-9	Sequence 9, Appl
52	13	52.0	4	6	US-10-609-019-5	Sequence 5, Appl
53	13	52.0	4	6	US-10-778-253-26	Sequence 26, Appl
54	13	52.0	4	6	US-10-778-253-28	Sequence 28, Appl
55	13	52.0	4	6	US-10-050-425-1	Sequence 1, Appl
56	13	52.0	4	6	US-10-050-425-2	Sequence 2, Appl
57	13	52.0	4	6	US-10-052-832-1	Sequence 1, Appl
58	13	52.0	4	6	US-10-052-832-2	Sequence 2, Appl
59	13	52.0	4	6	US-10-628-391-2	Sequence 2, Appl
60	13	52.0	4	6	US-10-138-935A-26	Sequence 26, Appl
61	13	52.0	4	6	US-10-138-935A-27	Sequence 27, Appl
62	13	52.0	4	6	US-10-660-118A-1	Sequence 1, Appl
63	13	52.0	4	6	US-10-807-807-1279	Sequence 1279, Ap
64	13	52.0	4	6	US-10-808-187-1279	Sequence 1279, Ap
65	13	52.0	4	6	US-10-808-121-1279	Sequence 1279, Ap

ALIGNMENTS

RESULT 1
PCT-US04-10121-1
; Sequence 1, Application PC/TUS0410121
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN INC.
; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; TITLE OF INVENTION: METHODS FOR NEURAL DIFFERENTIATION OF EMBRYONIC STEM
; TITLE OF INVENTION: CELLS USING PROTEASE PASSAGING TECHNIQUES
; FILE REFERENCE: 18377-0031
; CURRENT APPLICATION NUMBER: PCT/US04/10121
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,090
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO. 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
PCT-US04-10121-1

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

Db 1 GPRP 4
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RESULT 2

PCT-US04-16828-4

; Sequence 4, Application PC/TUS0416828
; GENERAL INFORMATION:
; APPLICANT: University of Texas
; TITLE OF INVENTION: Micropositioning Cells for Tissue
; FILE REFERENCE: 21105.0003P1
; CURRENT APPLICATION NUMBER: PCT/US04/16828
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: 60/474,574
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: synthetic construct

PCT-US04-16828-4

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0

Qy 1 GPRP 4
Db 1 GPRP 4
||||

RESULT 3

PCT-US03-40762-1

; Sequence 1, Application PC/TUS0340762
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN, INC.
; TITLE OF INVENTION: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; FILE REFERENCE: 18377-0028
; CURRENT APPLICATION NUMBER: PCT/US03/40762
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: 60/434,786
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

PCT-US03-40762-1

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0

Qy 1 GPRP 4
Db 1 GPRP 4
||||

RESULT 4

US-10-489-804-331

; Sequence 331, Application US/10489804
; GENERAL INFORMATION:

; APPLICANT: OREGON HEALTH AND SCIENCE UNIVERSITY
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Bulter, Andrew
; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Screen for Agents
; FILE REFERENCE: 899-68036
; CURRENT APPLICATION NUMBER: US/10/489,804
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: PCT/US02/30533
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 60/392,109
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/324,406
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 331
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide variation
; OTHER INFORMATION: US-10-489-804-331

Query Match 72.0%; Score 18; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0

Qy 1 GPR 3
Db 1 GPR 3
||||

RESULT 5

US-10-477-712B-62

; Sequence 62, Application US/10477712B
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: A Method for Producing A Peptide
; FILE REFERENCE: OXA-0213
; CURRENT APPLICATION NUMBER: US/10/477,712B
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: JP 2001-147341
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 62
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a cleavage sequence for thrombin

US-10-477-712B-62

Query Match 72.0%; Score 18; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0

Qy 1 GPR 3
Db 1 GPR 3
||||

RESULT 6

US-10-459-030B-2

; Sequence 2, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter

; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula I
US-10-459-030B-2

Query Match 72.0%; Score 18; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 1 GPR 3

RESULT 7
US-10-651-584C-90
; Sequence 90, Application US/10651584C
; GENERAL INFORMATION:
; APPLICANT: Lauermann, Vit
; TITLE OF INVENTION: Targeted release
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/651,584C
; CURRENT FILING DATE: 2003-08-30
; NUMBER OF SEQ ID NOS: 111
; SEQ ID NO 90
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: mammalian, peptide specifically cleavable by a reagent produced by a target cell
US-10-651-584C-90

Query Match 72.0%; Score 18; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 1 GPR 3

RESULT 8
US-09-804-733E-24
; Sequence 24, Application US/09804733E
; GENERAL INFORMATION:
; APPLICANT: WANG, QI ET AL.
; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING REPEATING UNITS
; FILE REFERENCE: MONS:016US
; CURRENT APPLICATION NUMBER: US/09/804,733E
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,990
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-804-733E-24

Query Match 72.0%; Score 18; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 2 GPR 4

RESULT 9
US-10-459-030B-4
; Sequence 4, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula I
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-4

Query Match 72.0%; Score 18; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
DB 1 GPR 3

RESULT 10
US-10-821-240A-151
; Sequence 151, Application US/10821240A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/821,240A
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 10/028,075
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 151
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sptrembl/09UCG8/09UCG8
US-10-821-240A-151

Query Match 72.0%; Score 18; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
Db 2 GPR 4

RESULT 11

US-10-720-831-5
; Sequence 5, Application US/10720831
; GENERAL INFORMATION:
; APPLICANT: Berg, Richard A
; Toman, David P
; Wallace, Donald
; TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COLLAGEN CORPORATION
; STREET: 2500 Faber Place
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/720,831
; FILING DATE: 24-Nov-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,774
; FILING DATE: 22-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rafayko, Kathi L
; REGISTRATION NUMBER: 36,644
; REFERENCE/DOCKET NUMBER: 94-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 354-4642
; TELEFAX: (415) 354-4752
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-720-831-5

Query Match 72.0%; Score 18; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
Db 2 GPR 4

RESULT 12

US-60-548-401-3581
; GENERAL INFORMATION:
; APPLICANT: Sidelman, Zvi
; TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
; FILE REFERENCE: 27567
; CURRENT APPLICATION NUMBER: US/60/548,401
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 4000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3581

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-60-548-401-3581

Query Match 68.0%; Score 17; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPPF 4

RESULT 13

PCT-US04-10121-4
; Sequence 4, Application PC/TUS0410121
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN INC.
; TITLE OF INVENTION: METHODS FOR NEURAL DIFFERENTIATION OF EMBRYONIC STEM
; TITLE OF INVENTION: CELLS USING PROTEASE PASSAGING TECHNIQUES
; FILE REFERENCE: 18377-0031
; CURRENT APPLICATION NUMBER: PCT/US04/10121
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,090
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
PCT-US04-10121-4

Query Match 64.0%; Score 16; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 6.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
|||
Db 2 PKP 4

RESULT 14

PCT-US03-40762-4
; Sequence 4, Application PC/TUS0340762
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN, INC.
; TITLE OF INVENTION: METHODS FOR NEURAL DIFFERENTIATION OF EMBRYONIC STEM
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL CELL PRODUCTION AND
; FILE REFERENCE: 18377-0028
; CURRENT APPLICATION NUMBER: PCT/US03/40762
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: 60/434,786
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US03-40762-4

Query Match 64.0%; Score 16; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 6.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRP 4
 | : |
 Db 2 PKP 4

RESULT 15
 US-10-686-884-9
 ; Sequence 9, Application US/10686884
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris, Jennifer L.
 ; APPLICANT: Backes, Bradley J.
 ; APPLICANT: Ellman, Jonathan A.
 ; APPLICANT: Craik, Charles S.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Profiling of Protease Specificity Using Combinatorial
 ; TITLE OF INVENTION: Fluorogenic Substrate Libraries
 ; FILE REFERENCE: 18062G-003211US
 ; CURRENT APPLICATION NUMBER: US/10/686,884
 ; CURRENT FILING DATE: 2003-10-15
 ; PRIOR APPLICATION NUMBER: US 60/209,274
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: US 09/866,132
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: WO PCT/US01/17265
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 4
 ; TYPE: PRP
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:tetrapeptide
 ; OTHER INFORMATION: substrate thrombin-susceptible sequence
 US-10-686-884-9

Query Match 60.0%; Score 15; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 6.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
 | : |
 Db 2 GPK 4

RESULT 16
 US-60-548-401-486
 ; Sequence 486, Application US/60548401
 ; GENERAL INFORMATION:
 ; APPLICANT: Sidelman, Zvi
 ; TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
 ; FILE REFERENCE: 27567
 ; CURRENT APPLICATION NUMBER: US/60/548,401
 ; CURRENT FILING DATE: 2004-03-01
 ; NUMBER OF SEQ ID NOS: 4000
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 486
 ; LENGTH: 3
 ; TYPE: PRP
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-60-548-401-486

Query Match 56.0%; Score 14; DB 7; Length 3;
 Best Local Similarity 66.7%; Pred. No. 6.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRP 4

Db 1 PNP 3

RESULT 17
 PCT-US04-04137-36
 ; Sequence 36, Application PC/TUS0404137
 ; GENERAL INFORMATION:
 ; APPLICANT: Health Matrix Sciences
 ; APPLICANT: Mitts, Thomas
 ; APPLICANT: Jimenez, Felipe
 ; TITLE OF INVENTION: ELASTIN DIGEST COMPOSITIONS AND METHODS UTILIZING SAME
 ; FILE REFERENCE: 126595.102
 ; CURRENT APPLICATION NUMBER: PCT/US04/04137
 ; CURRENT FILING DATE: 2004-02-13
 ; PRIOR APPLICATION NUMBER: 60/447461
 ; PRIOR FILING DATE: 2003-02-14
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 36
 ; LENGTH: 4
 ; TYPE: PRP
 ; ORGANISM: BOVINE
 ; PCT-US04-04137-36

Query Match 56.0%; Score 14; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 6.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
 | : |
 Db 1 GPQ 3

RESULT 18
 PCT-US04-11167-158
 ; Sequence 158, Application PC/TUS0411167
 ; GENERAL INFORMATION:
 ; APPLICANT: GILCHRIST, ANNETTE
 ; APPLICANT: HAMM, HEIDI
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
 ; TITLE OF INVENTION: SIGNALING
 ; FILE REFERENCE: 2661-102
 ; CURRENT APPLICATION NUMBER: PCT/US04/11167
 ; CURRENT FILING DATE: 2004-04-16
 ; PRIOR APPLICATION NUMBER: US 10/411336
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: US 09/852910
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: US 60/275472
 ; PRIOR FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 158
 ; LENGTH: 4
 ; TYPE: PRP
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: G alpha t library linker sequence
 PCT-US04-11167-158

Query Match 56.0%; Score 14; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 6.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
 | : |
 Db 2 GPQ 4

RESULT 19
 US-09-852-910B-158
 ; Sequence 158, Application US/09852910B

```
; GENERAL INFORMATION:
; APPLICANT: GILCHRIST, ANNETTE
; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910B
; PRIOR FILING DATE: 2001-05-11
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G alpha t library linker sequence
US-09-852-910B-158

Query Match          56.0%; Score 14; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 6.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
   |||
Db 2 GPQ 4

RESULT 20
US-10-778-253-36
; Sequence 36, Application US/10778253
; GENERAL INFORMATION:
; APPLICANT: Health Matrix Sciences
; APPLICANT: Mitts, Thomas
; APPLICANT: Jimenez, Felipe
; TITLE OF INVENTION: ELASTIN DIGEST COMPOSITIONS AND METHODS UTILIZING SAME
; FILE REFERENCE: 126595.101
; CURRENT APPLICATION NUMBER: US/10/778,253
; CURRENT FILING DATE: 2004-02-13
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 4
; TYPE: PRT
; ORGANISM: BOVINE
US-10-778-253-36

Query Match          56.0%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 6.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
   |||
Db 1 GPQ 3

RESULT 21
US-60-548-401-518
; Sequence 518, Application US/60548401
; GENERAL INFORMATION:
; APPLICANT: Sidelman, Zvi
; TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
; FILE REFERENCE: 27567
; CURRENT APPLICATION NUMBER: US/60/548,401
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 4000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 518
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-60-548-401-3546

Query Match          52.0%; Score 13; DB 7; Length 2;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
   ||
Db 1 GP 2

RESULT 24
US-60-548-401-3550
; Sequence 3550, Application US/60548401
```

```
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-60-548-401-518

Query Match          56.0%; Score 14; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRP 4
   |||
Db 2 PNP 4

RESULT 22
US-60-548-401-519
; Sequence 519, Application US/60548401
; GENERAL INFORMATION:
; APPLICANT: Sidelman, Zvi
; TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
; FILE REFERENCE: 27567
; CURRENT APPLICATION NUMBER: US/60/548,401
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 4000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 519
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-60-548-401-519

Query Match          56.0%; Score 14; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRP 4
   |||
Db 1 PNP 3

RESULT 23
US-60-548-401-3546
; Sequence 3546, Application US/60548401
; GENERAL INFORMATION:
; APPLICANT: Sidelman, Zvi
; TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
; FILE REFERENCE: 27567
; CURRENT APPLICATION NUMBER: US/60/548,401
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 4000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3546
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-60-548-401-3546

Query Match          52.0%; Score 13; DB 7; Length 2;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
   ||
Db 1 GP 2

RESULT 24
US-60-548-401-3550
; Sequence 3550, Application US/60548401
```

```
; GENERAL INFORMATION:
; APPLICANT: Sidelman, Zvi
; TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
; FILE REFERENCE: 27567
; CURRENT APPLICATION NUMBER: US/60/548,401
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 4000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3550
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-60-548-401-3550

Query Match          52.0%; Score 13; DB 7; Length 2;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GP 2
      ||
DB      1 GP 2

RESULT 25
PCT-US04-02004-70
; Sequence 70, Application PC/TUS0402004
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Abeta Binding Molecules
; FILE REFERENCE: X-16088
; CURRENT APPLICATION NUMBER: PCT/US04/02004
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/446380
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: substituted CDR
PCT-US04-02004-70

Query Match          52.0%; Score 13; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GP 2
      ||
DB      1 GP 2

RESULT 26
PCT-US03-33658A-26
; Sequence 26, Application PC/TUS0333658A
; GENERAL INFORMATION:
; APPLICANT: Villanueva, Julie M.
; APPLICANT: Quirk, Stephen
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: Compounds that Bind P2Y2 or P2Y1 Receptors
; FILE REFERENCE: 1443.029W01
; CURRENT APPLICATION NUMBER: PCT/US03/33658A
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 10/320,731
; PRIOR FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic example of peptide modulator of P2Y2 or P2Y1 receptors
PCT-US03-33658A-26

Query Match          52.0%; Score 13; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GP 2
      ||
DB      1 GP 2

RESULT 27
US-10-682-011-16
; Sequence 16, Application US/10682011
; GENERAL INFORMATION:
; APPLICANT: Alibhai, Murtaza
; APPLICANT: Rydel, Timothy
; TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
; FILE REFERENCE: 38-21 (51842)B
; CURRENT APPLICATION NUMBER: US/10/682,011
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/755,274
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 3
; TYPE: PRT
; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: Protein
; LOCATION: (1)..(3)
; OTHER INFORMATION: Linker Sequence
US-10-682-011-16

Query Match          52.0%; Score 13; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GP 2
      ||
DB      1 GP 2

RESULT 28
US-60-548-401-3561
; Sequence 3561, Application US/60548401
; GENERAL INFORMATION:
; APPLICANT: Sidelman, Zvi
; TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
; FILE REFERENCE: 27567
; CURRENT APPLICATION NUMBER: US/60/548,401
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 4000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3561
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-60-548-401-3561

Query Match          52.0%; Score 13; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GP 2
      ||
DB      2 GP 3
```


Best Local Similarity 100.0%; Pred. No. 6.2e+05; DB 1; Length 4;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GP 2
 Db 1 GP 2

RESULT 34
 PCT-US04-04137-28
 ; Sequence 28, Application PC/TUS0404137
 ; GENERAL INFORMATION:
 ; APPLICANT: Health Matrix Sciences
 ; APPLICANT: Mitts, Thomas
 ; APPLICANT: Jimenez, Felipe
 ; TITLE OF INVENTION: ELASTIN DIGEST COMPOSITIONS AND METHODS UTILIZING SAME
 ; FILE REFERENCE: 126595.102
 ; CURRENT APPLICATION NUMBER: PCT/US04/04137
 ; CURRENT FILING DATE: 2004-02-13
 ; PRIOR APPLICATION NUMBER: 60/447461
 ; PRIOR FILING DATE: 2003-02-14
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 28
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 PCT-US04-04137-28

Query Match 52.0%; Score 13; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GP 2
 Db 1 GP 2

RESULT 35
 PCT-US03-41269-81
 ; Sequence 81, Application PC/TUS0341269
 ; GENERAL INFORMATION:
 ; APPLICANT: TRANSGENRES, LLC
 ; APPLICANT: The Board of Supervisors of Louisiana State University and
 ; APPLICANT: Agricultural and Mechanical College
 ; TITLE OF INVENTION: Vaccine Production Using Transposon Based Vectors
 ; FILE REFERENCE: 51687-0270WP (51687-295831)
 ; CURRENT APPLICATION NUMBER: PCT/US03/41269
 ; CURRENT FILING DATE: 2003-12-24
 ; PRIOR APPLICATION NUMBER: US 10/609,019
 ; PRIOR FILING DATE: 2003-06-26
 ; PRIOR APPLICATION NUMBER: US 60/441,392
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,377
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,502
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,405
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,447
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,381
 ; PRIOR FILING DATE: 2003-01-21
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 81
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 PCT-US03-41269-81

Query Match 52.0%; Score 13; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GP 2
 Db 1 GP 2

RESULT 36
 PCT-US04-11167-171
 ; Sequence 171, Application PC/TUS0411167
 ; GENERAL INFORMATION:
 ; APPLICANT: GILCHRIST, ANNETTE
 ; APPLICANT: HAMM, HEIDI
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 2661-102
 ; CURRENT APPLICATION NUMBER: PCT/US04/11167
 ; CURRENT FILING DATE: 2004-04-16
 ; PRIOR APPLICATION NUMBER: US 10/411336
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: US 09/852910
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: US 60/275472
 ; PRIOR FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 171
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: G alpha 11 library linker sequence
 PCT-US04-11167-171

Query Match 52.0%; Score 13; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 6.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PRP 4
 Db 2 PSP 4

RESULT 37
 PCT-US03-41261-81
 ; Sequence 81, Application PC/TUS0341261
 ; GENERAL INFORMATION:
 ; APPLICANT: TRANSGENRES, LLC
 ; APPLICANT: The Board of Supervisors of Louisiana State University and
 ; APPLICANT: Agricultural and Mechanical College
 ; TITLE OF INVENTION: Production of Multimeric Proteins
 ; FILE REFERENCE: 51687-0230WP (51687-295698)
 ; CURRENT APPLICATION NUMBER: PCT/US03/41261
 ; CURRENT FILING DATE: 2003-12-24
 ; PRIOR APPLICATION NUMBER: US 60/441,381
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,447
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,405
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,502
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,377
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/441,392
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 10/609,019
 ; PRIOR FILING DATE: 2003-06-26
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 81

; LENGTH: 4
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US03-41261-81

Query Match 52.0%; Score 13; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
Db 1 GP 2

RESULT 38

PCT-US03-41335-26
; Sequence 26, Application PC/TUS0341335
; GENERAL INFORMATION:
; APPLICANT: TRANSGENES, LLC
; APPLICANT: The Board of Supervisors fo Louisiana State University and
; APPLICANT: Agricultural and Mechanical College
; TITLE OF INVENTION: Administration of Transposon-Based Vectors to Reproductive Organs
; FILE REFERENCE: 51687-0280WP (51687-295699)
; CURRENT APPLICATION NUMBER: PCT/US03/41335
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/441,381
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,447
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,405
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,502
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,392
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,377
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 10/609,019
; PRIOR FILING DATE: 2003-06-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US03-41335-26

Query Match 52.0%; Score 13; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
Db 1 GP 2

RESULT 39

PCT-US04-10121-2
; Sequence 2, Application PC/TUS0410121
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN INC.
; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; TITLE OF INVENTION: METHODS FOR NEURAL DIFFERENTIATION OF EMBRYONIC STEM
; TITLE OF INVENTION: CELLS USING PROTEASE PASSAGING TECHNIQUES
; FILE REFERENCE: 18377-0031
; CURRENT APPLICATION NUMBER: PCT/US04/10121
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,090
; PRIOR FILING DATE: 2003-03-31

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
PCT-US04-10121-2

Query Match 52.0%; Score 13; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
Db 1 GP 2

RESULT 40

PCT-US03-40762-2
; Sequence 2, Application PC/TUS0340762
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN, INC.
; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL CELL PRODUCTION AND
; TITLE OF INVENTION: STABILIZATION
; FILE REFERENCE: 18377-0028
; CURRENT APPLICATION NUMBER: PCT/US03/40762
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: 60/434,786
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US03-40762-2

Query Match 52.0%; Score 13; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
||
Db 1 GP 2

RESULT 41

US-09-852-910B-171
; Sequence 171, Application US/09852910B
; GENERAL INFORMATION:
; APPLICANT: GILCHRIST, ANNETTE
; APPLICANT: HAMM, HEIDI
; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: SIGNALING
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/275472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: G alpha 11 library linker sequence
US-09-852-910B-171

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRP 4
DB 2 PSP 4

RESULT 42

US-09-421-545-1
; Sequence 1, Application US/09421545
; GENERAL INFORMATION:
; APPLICANT: Mundy, Gregory
; APPLICANT: Garrett, I. Ross
; APPLICANT: Rossini, G.
; TITLE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR
; TITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
; FILE REFERENCE: 432722002621
; CURRENT APPLICATION NUMBER: US/09/421,545
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/361,775
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 09/113,947
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRP
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: a.a. portion of ALLM compound as proteasome
; OTHER INFORMATION: inhibitor
US-09-421-545-1

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
DB 1 GP 2

RESULT 43

US-09-421-545-2
; Sequence 2, Application US/09421545
; GENERAL INFORMATION:
; APPLICANT: Mundy, Gregory
; APPLICANT: Garrett, I. Ross
; APPLICANT: Rossini, G.
; TITLE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR
; TITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
; FILE REFERENCE: 432722002621
; CURRENT APPLICATION NUMBER: US/09/421,545
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/361,775
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 09/113,947
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRP
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: a.a. portion of ALLM compound as proteasome
; OTHER INFORMATION: inhibitor

US-09-421-545-2

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
DB 1 GP 2

RESULT 44

US-09-558-973-1
; Sequence 1, Application US/09558973
; GENERAL INFORMATION:
; APPLICANT: Mundy, Gregory
; APPLICANT: Garrett, I. Ross
; APPLICANT: Rossini, G.
; TITLE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR
; TITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
; FILE REFERENCE: 432722002622
; CURRENT APPLICATION NUMBER: US/09/558,973
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/421,545
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/361,775
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 09/113,947
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRP
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: a.a. portion of ALLM compound as proteasome
; OTHER INFORMATION: inhibitor
US-09-558-973-1

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GP 2
DB 1 GP 2

RESULT 45

US-09-558-973-2
; Sequence 2, Application US/09558973
; GENERAL INFORMATION:
; APPLICANT: Mundy, Gregory
; APPLICANT: Garrett, I. Ross
; APPLICANT: Rossini, G.
; TITLE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR
; TITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
; FILE REFERENCE: 432722002622
; CURRENT APPLICATION NUMBER: US/09/558,973
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/421,545
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/361,775
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 09/113,947
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRP
; ORGANISM: Unknown

;
; FEATURE:
; OTHER INFORMATION: a.a. portion of ALLM compound as proteasome
; OTHER INFORMATION: inhibitor
US-09-558-973-2

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GP 2
||
Db 1 GP 2

RESULT 46
US-09-429-578A-18
; Sequence 18, Application US/09429578A
; GENERAL INFORMATION:
; APPLICANT: Perrick, David A.
; TITLE OF INVENTION: Novel Compositions and Methods of Screening for T-Cell
; TITLE OF INVENTION: and B-Cell Activation Modulators
; FILE REFERENCE: 021044-0057100S
; CURRENT APPLICATION NUMBER: US/09/429,578A
; CURRENT FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 60/106,187
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: peptide
US-09-429-578A-18

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GP 2
||
Db 1 GP 2

RESULT 47
US-09-310-685-23
; Sequence 23, Application US/09310685
; GENERAL INFORMATION:
; APPLICANT: Lamb, Jonathan R
; APPLICANT: Dallman, Margaret J
; APPLICANT: Hoyne, Gerard F
; TITLE OF INVENTION: Notch
; FILE REFERENCE: 674525-2001
; CURRENT APPLICATION NUMBER: US/09/310,685
; CURRENT FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: GB 9623326.8
; PRIOR FILING DATE: 1996-11-07
; PRIOR APPLICATION NUMBER: GB 9715674.9
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: GB 9719350.2
; PRIOR FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: PCT/GB97/03058
; PRIOR FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-310-685-23

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GP 2
||
Db 3 GP 4

RESULT 48
US-09-695-807-1
; Sequence 1, Application US/09695807
; GENERAL INFORMATION:
; APPLICANT: Mundy, Gregory R.
; APPLICANT: Garrett, I. Ross
; APPLICANT: Rossini, G.
; TITLE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR
; TITLE OF INVENTION: STIMULATING BONE GROWTH
; FILE REFERENCE: 432722002623
; CURRENT APPLICATION NUMBER: US/09/695,807
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 09/421,545
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/361,775
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 09/113,947
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: a.a. portion of ALLM compound as proteasome
; OTHER INFORMATION: inhibitor
US-09-695-807-1

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GP 2
||
Db 1 GP 2

RESULT 49
US-09-695-807-2
; Sequence 2, Application US/09695807
; GENERAL INFORMATION:
; APPLICANT: Mundy, Gregory R.
; APPLICANT: Garrett, I. Ross
; APPLICANT: Rossini, G.
; TITLE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR
; TITLE OF INVENTION: STIMULATING BONE GROWTH
; FILE REFERENCE: 432722002623
; CURRENT APPLICATION NUMBER: US/09/695,807
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 09/421,545
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/361,775
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 09/113,947
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

; OTHER INFORMATION: a.a. portion of ALLM compound as proteasome
; OTHER INFORMATION: inhibitor
US-09-695-807-2

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred.No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GP 2
||
Db 1 GP 2

RESULT 50
US-09-592-695D-48
; Sequence 48, Application US/09592695D
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas J.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: Structured Peptide Scaffold For Displaying Turn
; TITLE OF INVENTION: Libraries On Phage
; FILE REFERENCE: 11669.116USUI
; CURRENT APPLICATION NUMBER: US/09/592,695D
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 48
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: turn peptide
US-09-592-695D-48

Query Match 52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred.No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GP 2
||
Db 1 GP 2

Search completed: September 7, 2004, 19:33:57
Job time : 60 secs

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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:22:37 ; Search time 15 Seconds

(without alignments)
25.651 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

1: PIR.78.*

2: PIR1.*

3: PIR2.*

4: PIR3.*

5: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	52.0	4	2 PT0675	T-cell receptor be
2	12	48.0	4	2 A02147	phagocytosis-stimu
3	7	28.0	3	3 RHTDFO	thyroliberin - Bom
4	7	28.0	3	3 RHPGT	thyroliberin - pig
5	7	28.0	3	3 PHSHT	thyroliberin - she
6	7	28.0	3	3 A92971	thyroliberin - eas
7	7	28.0	3	3 A33802	thyrotropin-releas
8	7	28.0	3	3 A43391	TRH-like tripeptid
9	7	28.0	3	3 I78890	tyrosine protein k
10	7	28.0	4	2 A32039	tyrosine-melanocyt
11	7	28.0	4	2 PL0140	carbon-monoxide de
12	7	28.0	4	2 S53508	starvation-induced
13	7	28.0	4	2 SI7255	ribosomal protein
14	7	28.0	4	2 A34626	RFCH-related neuro
15	7	28.0	4	2 I51049	metallothionein-A
16	7	28.0	4	2 PT0240	Ig heavy chain CRD
17	7	28.0	4	2 I54357	schwannomin - mous
18	6	24.0	3	3 GKHU	growth-modulating
19	6	24.0	3	3 A50898	Bursin - chicken
20	6	24.0	3	3 A23751	spinal cord peptid
21	6	24.0	3	3 B23751	spinal cord peptid
22	6	24.0	3	3 PT0636	T-cell receptor be
23	6	24.0	3	3 PT0571	T-cell receptor be
24	6	24.0	4	1 ECXAA	antho-Rfamidae neur
25	6	24.0	4	2 T30569	hypothetical prote
26	6	24.0	4	2 I38888	Col intron 16 prot
27	6	24.0	4	2 A25844	antho-RF amide neu
28	6	24.0	4	2 A32480	achatin-I - giant
29	6	24.0	4	2 S39390	myosin-light-chain

30 6 24.0 4 2 PT0271
31 6 24.0 4 2 S43959
32 6 24.0 4 2 A53284
33 6 24.0 4 2 B53284
34 6 24.0 4 2 PT0633
35 6 24.0 4 2 PT0711
36 6 24.0 4 2 PT0698
37 6 24.0 4 2 PT0677
38 6 24.0 4 2 PT0706
39 6 24.0 4 2 PT0721
40 6 24.0 4 2 PT0566
41 6 24.0 4 2 S47552
42 6 24.0 4 2 S09478
43 5 20.0 3 3 A22565
44 5 20.0 3 3 PQ0010
45 5 20.0 4 2 EGNK
46 5 20.0 4 2 D41654
47 5 20.0 4 2 I40870
48 5 20.0 4 2 A35779
49 5 20.0 4 2 A60418
50 5 20.0 4 2 I61883
51 5 20.0 4 2 I37013
52 5 20.0 4 2 I84439
53 2 8.0 3 3 S1894
54 2 8.0 3 3 E37196
55 2 8.0 3 3 F37196
56 2 8.0 3 2 PL0146
57 2 8.0 4 2 I40505
58 2 8.0 4 2 I40804
59 2 8.0 4 2 T46627
60 2 8.0 4 2 JQ1273
61 2 8.0 4 2 E44823
62 2 8.0 4 2 PT0534
63 1 4.0 4 2 A48360
64 1 4.0 4 2 I57745
65 0 0.0 3 3 I50412

ALIGNMENTS

RESULT 1

PT0675 T-cell receptor beta chain V-D-J region (140-14C) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0675

R;Reeney, A.J.
J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277501; PMID:1711558

A;Accession: PT0675

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-4 <PEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 52.0%; Score 13; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GP 2

Db 3 GP 4

RESULT 2

A02147 phagocytosis-stimulating peptide (tuftsin) - human

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Feb-1994

C;Accession: A02147

R;Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
 Biochem. Biophys. Res. Commun. 47, 172-179, 1972
 A;Title: The characteristics, isolation and synthesis of the phagocytosis stimulating peptide
 A;Reference number: A02147; PMID:4112769
 A;Accession: A02147
 A;Molecule type: protein
 A;Residues: 1-4 <NIS>
 A;Note: a peptide having the same structure, physical properties, and biological activities as
 R;Fidalgo, B.V.; Najjar, V.A.
 Biochemistry 6, 3385-3392, 1967
 A;Reference number: A37502; PMID:4169272
 A;Contents: annotation; immunoglobulin class
 C;Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils
 C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 48.0%; Score 12; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 3
 Db 3 P 4

RESULT 3
 RHPTO
 thyroliberin - Bombina orientalis
 C;Species: Bombina orientalis
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A90919; A01415
 R;Yasukura, T.; Nakajima, T.
 Chem. Pharm. Bull. 23, 3301-3303, 1975
 A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
 A;Reference number: A90919; PMID:76138399; PMID:815011
 A;Accession: A90919
 A;Molecule type: protein
 A;Residues: 1-3 <YAS>
 C;Superfamily: thyroliberin precursor
 C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.0%; Score 7; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
 Db 3 P 3

RESULT 4
 RHPTG
 thyroliberin - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A01415
 R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.
 Biochemistry 9, 1103-1106, 1970
 A;Title: Structure of porcine thyrotropin releasing hormone.
 A;Reference number: A90560; PMID:70136150; PMID:4984938
 A;Accession: A01415
 A;Molecule type: protein
 A;Residues: 1-3 <NAI>
 R;Boiler, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 37, 705-710, 1969
 A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing hormone.
 A;Reference number: A90167; PMID:70039904; PMID:4982117
 A;Contents: annotation
 A;Note: biological activities and Rf values (in 17 chromatographic systems) of the synthetic
 C;Superfamily: thyroliberin precursor
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.0%; Score 7; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
 Db 3 P 3

RESULT 5
 RHSTT
 thyroliberin - sheep
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A93750; A01415
 R;Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
 Org. Mass Spectrom. 5, 221-228, 1971
 A;Title: The elucidation of the primary structure of the hypothalamic thyrotropin stimulating
 A;Reference number: A93750
 A;Accession: A93750
 A;Molecule type: protein
 A;Residues: 1-3 <DES>
 R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
 Nature 226, 321-325, 1970
 A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
 A;Reference number: A93161; PMID:70163386; PMID:4985794
 A;Contents: annotation
 A;Note: physicochemical characteristics and biological activities of the natural and synthetic
 C;Superfamily: thyroliberin precursor
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.0%; Score 7; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
 Db 3 P 3

RESULT 6
 A92971
 thyroliberin - eastern newt (tentative sequence)
 C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A92971; A01415
 R;Grimm-Jorgensen, Y.; McKelvy, J.F.
 J. Neurochem. 23, 471-478, 1974
 A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain
 A;Reference number: A92971; PMID:75035605; PMID:4214528
 A;Accession: A92971
 A;Molecule type: protein
 A;Residues: 1-3 <GRI>
 A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyrotropin
 C;Superfamily: thyroliberin precursor
 C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.0%; Score 7; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
 Db 3 P 3

RESULT 7
 A33802
 thyrotropin-releasing hormone-like peptide - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: A33802
 R:Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.
 J. Biol. Chem. 264, 7788-7791, 1989
 A:Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate comp
 A:Reference number: A33802; MUID:89255196; PMID:2498305
 A:Accession: A33802
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-3 <COC>
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3/Modified site: amidated carboxyl end (Pro) #status experimental

 Query Match 28.0%; Score 7; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 P 2
 Db 3 P 3

 RESULT 8
 A43391
 TRH-like tripeptide - alfalfa
 C:Species: Medicago sativa (alfalfa)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: A43391
 R:Lackey, D.B.
 J. Biol. Chem. 267, 17508-17511, 1992
 A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-
 A:Reference number: A43391; MUID:92388092; PMID:1517203
 A:Accession: A43391
 A:Molecule type: protein
 A:Residues: 1-3 <IAC>
 C:Keywords: amidated carboxyl end; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3/Modified site: amidated carboxyl end (Pro) #status experimental

 Query Match 28.0%; Score 7; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 P 2
 Db 3 P 3

 RESULT 9
 I78890
 tyrosine protein kinase - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: I78890
 R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
 Oncogene 9, 3437-3448, 1994
 A:Title: Two distinct protein isoforms are encoded by nt, a csk-related tyrosine protei
 A:Reference number: 158407; MUID:95060800; PMID:7570703
 A:Accession: I78890
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-3 <RES>
 A:Cross-references: GB:L33339; NID:g609536; PIDN:AA64432.1; PID:g609538
 C:Genetics:
 A:Gene: p52ntk

Query Match 28.0%; Score 7; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 P 2
 Db 2 P 2

 RESULT 10
 A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
 C:Accession: A32039
 R:Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989
 A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1
 A:Reference number: A32039; MUID:89123285; PMID:2563371
 A:Accession: A32039
 A:Molecule type: protein
 A:Residues: 1-4 <HOR>
 A:Experimental source: brain
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

 Query Match 28.0%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 P 2
 Db 2 P 2

 RESULT 11
 PL0140
 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena
 C:Species: Pseudomonas carboxydohydrogena
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
 C:Accession: PL0140
 R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
 Arch. Microbiol. 152, 335-341, 1989
 A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotropt
 A:Reference number: PL0138; MUID:90055678; PMID:2818128
 A:Accession: PL0140
 A:Molecule type: protein
 A:Residues: 1-4 <KRA>
 C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
 C:Keywords: oxidoreductase

 Query Match 28.0%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 P 2
 Db 4 P 4

 RESULT 12
 S53508
 starvation-induced ribonuclease - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 C:Accession: S53508
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995
 A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribor
 A:Reference number: S53506; MUID:95201242; PMID:7894013
 A:Accession: S53508
 A:Status: preliminary

A;Molecule type: protein
A;Residues: 1-4 <KOE>

Query Match 28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
|
Db 2 P 2

RESULT 13

S17255 ribosomal protein Ym11, mitochondrial, questionable - yeast (*Saccharomyces cerevisiae*)

C;Species: *Saccharomyces cerevisiae*
A;Variety: strain 07173
C;Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
C;Accession: S17255

R;Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
FEBS Lett. 284, 51-56, 1991
A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from

A;Reference number: S17255; MUID:91285106; PMID:2060626
A;Accession: S17255

A;Molecule type: protein
A;Residues: 1-4 <GRO>

C;Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*
C;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
|
Db 4 P 4

RESULT 14

A34626

RPCH-related neuroptide - ferruginous spindle

C;Species: *Fusinus ferrugineus* (ferruginous spindle)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626

R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A;Title: A molluscan neuroptide related to the crustacean hormone, RPCH.

A;Reference number: A34626; MUID:90179762; PMID:2310394

A;Accession: A34626

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KUR>

C;Keywords: neuroptide

Query Match 28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
|
Db 2 P 2

RESULT 15

I51049

metallothionein-A - rainbow trout (fragment)

C;Species: *Oncorhynchus mykiss* (rainbow trout)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51049

R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A;Title: Structural and functional analysis of the rainbow trout (*Oncorhynchus mykiss*) met
A;Reference number: I51049; MUID:95324545; PMID:7601121

A;Accession: I51049

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-4 <OLS>

A;Cross-references: EMBL:X80181; NID:G1019799; PIDN:CAA56466.1; PID:G4379328

Query Match 28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
|
Db 3 P 3

RESULT 16

PT0240

Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0240

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0240

A;Molecule type: DNA

A;Residues: 1-4 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
|
Db 2 P 2

RESULT 17

I54357

schwannomin - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I54357

R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.

Hum. Mol. Genet. 3, 1075-1079, 1994

A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are cor
A;Reference number: I54357; MUID:95072570; PMID:7981675

A;Accession: I54357

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-4 <RES>

A;Cross-references: GB:L28838; NID:G454836; PIDN:AAA57150.1; PID:G601923

C;Genetics:

A;Gene: NF2

Query Match 28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 P 2
|
Db 2 P 2

RESULT 18

GKHU

growth-modulating peptide - human

C;Species: *Homo sapiens* (man)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A01421
R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; PMID:77162363; PMID:858556
A;Accession: A01421
A;Molecule type: protein
A;Status: preliminary
A;Residues: 1-3 <SCH>
C;Superfamily: unassigned animal peptides

Query Match 24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 1 G 1

RESULT 19
A60898
bursin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A60898
R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of b
A;Reference number: A60898; PMID:86122916; PMID:3484838
A;Accession: A60898
A;Molecule type: protein
A;Residues: 1-3 <AUD>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; hormone
F.3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 3 G 3

RESULT 20
A23751
spinal cord peptide SCP-4 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; PMID:85250425; PMID:4015098
A;Accession: A23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <HSI>
C;Superfamily: unassigned animal peptides

Query Match 24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 2 G 2

RESULT 21
B23751

spinal cord peptide SCP-5 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: B23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; PMID:85250425; PMID:4015098
A;Accession: B23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <HSI>
C;Superfamily: unassigned animal peptides

Query Match 24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 3 G 3

RESULT 22
PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0636
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; PMID:91277601; PMID:1711558
A;Accession: PT0636
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 3 G 3

RESULT 23
PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0571
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; PMID:91277601; PMID:1711558
A;Accession: PT0571
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 3 G 3

RESULT 24
 ECXAA
 C:Species: Anthopleura elegantissima
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
 C:Accession: A26666
 R:Grimmelikhuizen, C.J.P.; Graff, D.
 Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
 A:Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anemone
 A:Reference number: A26666; PMID:8702339; PMID:2879288
 A:Accession: A26666
 A:Molecule type: protein
 A:Residues: 1-4 <GRI>
 C:Comment: The function of this peptide is not known but it could act as a transmitter and
 C:Comment: Synthetic and natural peptides had identical properties.
 C:Superfamily: Rhamide neuropeptide
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:4/Modified site: amidated carboxyl end (Phe) #status experimental
 Query Match 24.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 G 1
 Db 2 G 2
 RESULT 25
 T30569
 C:Species: Emericella nidulans
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
 C:Accession: T30569
 R:Morrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
 Curr. Genet. 34, 379-385, 1998
 A:Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergillus
 A:Reference number: Z20869; PMID:99087906; PMID:9871120
 A:Accession: T30569
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <MOR>
 A:Cross-references: EMBL:Y15986; NID:e1285512; PID:e1218041; PIDN:CAA75927.1
 Query Match 24.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 G 1
 Db 2 G 2
 RESULT 26
 I38988
 C:Species: Podospora anserina
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
 C:Accession: I38988
 R:Cummings, D.J.; Michel, P.; McNally, K.L.
 Curr. Genet. 16, 381-406, 1989
 A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mi
 A:Reference number: A48327; PMID:90124722; PMID:2558609
 A:Accession: I38988
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-4 <CUM>
 A:Cross-references: GB:X55026; GB:M30937; GB:M61734
 C:Genetics:
 A:Genome: mitochondrion
 A:Genetic code: SGC3
 C:Keywords: mitochondrion
 Query Match 24.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 G 1
 Db 2 G 2
 RESULT 27
 A25844
 C:Species: Renilla koelikeri (Koeliker's sea pansy)
 C:Date: 21-May-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
 C:Accession: A25844
 R:Grimmelikhuizen, C.J.P.; Groeger, A.
 FEBS Lett. 211, 105-108, 1987
 A:Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renilla
 A:Reference number: A25844
 A:Accession: A25844
 A:Molecule type: protein
 A:Residues: 1-4 <GRI>
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:4/Modified site: amidated carboxyl end (Phe) #status experimental
 Query Match 24.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 G 1
 Db 2 G 2
 RESULT 28
 A32480
 C:Species: Achatina fulica (giant African snail)
 C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
 C:Accession: A32480
 R:Kamatani, Y.; Minakata, H.; Kenry, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun,
 Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
 A:Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru
 A:Reference number: A32480; PMID:89273551; PMID:2597281
 A:Accession: A32480
 A:Molecule type: protein
 A:Residues: 1-4 <KAM>
 A:Note: stereochemistry of the active form confirmed by chemical synthesis
 R:Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto,
 FEBS Lett. 307, 253-256, 1992
 A:Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro
 (H-Gly-Phe-Ala-Asp-OH)
 A:Reference number: A44691; PMID:92354723; PMID:1544179
 A:Contents: annotation; X-ray crystallography, 0.85 angstroms
 A:Note: achatin-II has L-phenylalanine
 C:Keywords: D-amino acid
 F:2/Modified site: D-phenylalanine (Phe) #status experimental
 Query Match 24.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 G 1
 Db 1 G 1
 RESULT 29
 S39390

myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - turkey (fragment)
C;Species: Meleagris gallopavo (common turkey)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 07-May-1999
C;Accession: S39390
R;Komatsu, H.; Ikebe, M.
Biochem. J. 296, 53-58, 1993
A;Title: Affinity labelling of smooth-muscle myosin light-chain kinase with 5'-[p-(fluoromethyl)phosphoryl]adenosine triphosphate (FM-ATP)
A;Reference number: S39390; MUID:94071941; PMID:8250857
A;Accession: S39390
A;Molecule type: protein
A;Residues: 1-4 <KOM>
A;Experimental source: gizzard
C;Keywords: phosphotransferase; smooth muscle

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 2 G 2

RESULT 30

PT0271
IG heavy chain CDR3 region (clone 3-103A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
A;Accession: PT0271
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J_H gene segments in the generation of the CDR3 region of the heavy chain of a monoclonal antibody
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0271
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 2 G 2

RESULT 31

S43959
Ig mu chain V region (clone 13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43959
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.
Nucleic Acids Res. 22, 1389-1393, 1994
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A;Reference number: S43956; MUID:94248036; PMID:8190629
A;Accession: S43959
A;Molecule type: DNA
A;Residues: 1-4 <WAG>
C;Keywords: immunoglobulin

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 4 G 4

RESULT 32

PT0633

A53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and J_H gene segments in the beta 2 chain of the T-cell receptor
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: A53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:G233916; PIDN:AAB19518.1; PID:G233917
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)
C;Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 1 G 1

RESULT 33

B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and J_H gene segments in the beta 2 chain of the T-cell receptor
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: B53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:G233916; PIDN:AAB19518.1; PID:G233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
Db 3 G 3

RESULT 34

PT0633
T-cell receptor beta chain V-D-J region (120-20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0633
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0633
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEF>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
|
Db 3 G 3

RESULT 35

PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0607
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <PE1>
A:Experimental source: newborn thymus, strain BALB/c, 120-2J
A:Accession: PT0674
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <PE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A:Accession: PT0678-
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <PE3>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A:Accession: PT0570
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <PE4>
A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A:Accession: PT0711

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <PE5>
A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C:Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
|
Db 3 G 3

RESULT 36

PT0698
T-cell receptor beta chain V-D-J region (126-1AH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
C:Accession: PT0546; PT0698; PT0583
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0546
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <PEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AH
A:Accession: PT0698
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <PE2>
A:Experimental source: newborn thymus, strain BALB/c, 135-1BP
A:Accession: PT0583

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <PE2>
A:Experimental source: newborn thymus, strain BALB/c, 135-1BP
A:Accession: PT0583

A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-4 <FE3>
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2C
C:Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
|
Db 4 G 4

RESULT 37

PT0677
T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0558; PT0677
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0558
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <PEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG
A:Accession: PT0677
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <PE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH
C:Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
|
Db 3 G 3

RESULT 38

PT0706
T-cell receptor beta chain V-D-J region (135-1DU) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0706
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0706
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <PEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
|
Db 3 G 3

RESULT 39

PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0721
J;Feeney, A.J.
J;Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0721
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
|
Db 4 G 4

RESULT 40

PT0566
T-cell receptor beta chain V-D-J region (141-1CH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0566
J;Feeney, A.J.
J;Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0566
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
|
Db 3 G 3

RESULT 41

S47552
ubiquitin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: S47552
R;Hubbard, M.J.; Carne, A.
Biochim. Biophys. Acta 1200, 191-196, 1994
A;Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
A;Reference number: S47552; MUID:94304928; PMID:8031840
A;Accession: S47552
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <HUB>

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
|
Db 3 G 3

RESULT 42

S09478
globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
N;Alternate names: 11S globulin alpha subunit gamma chain
C;Species: Cucurbita sp. (cucurbit)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C;Accession: S09478
R;Ohmiya, M.; Hara, I.; Matsubara, H.
Plant Cell Physiol. 21, 157-167, 1980
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
A;Reference number: S09066
A;Accession: S09478
A;Molecule type: protein
A;Residues: 1-4 <OHM>

Query Match 24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
|
Db 3 G 3

RESULT 43

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocionium coulteri) (fragment)
C;Species: Gastrocionium coulteri
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: A22565
A;Molecule type: protein
A;Residues: 1-3 <KLO>

Query Match 20.0%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
|
Db 3 R 3

RESULT 44

PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N;Alternate names: ficus latex peptide 3
C;Species: Ficus carica (common fig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PQ0010
R;Muryama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Accession: PQ0010
A;Molecule type: protein
A;Residues: 1-3 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
|
Db 3 R 3

RESULT 45

ECNK

cardioexcitatory neuropeptide FMRFamide - sunray clam

C;Species: Macrocallista nimbosa (sunray clam)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01426

R;Price, D.A.; Greenberg, M.J.

Science 197, 670-671, 1977

A;Title: Structure of a molluscan cardioexcitatory neuropeptide.

A;Reference number: A01426; MUID:77215956; PMID:877582

A;Accession: A01426

A;Molecule type: protein

A;Residues: 1-4 <PRI>

A;Note: the active peptide was also synthesized

C;Comment: This peptide was purified from pooled extracts of cerebral, pedal, and visceral action in molluscs; its exact physiological role is not yet established.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 5; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 R 3

Db 3 R 3

RESULT 46

D41654

hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)

C;Species: Haemophilus parainfluenzae

C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995

C;Accession: D41654

R;Kroll, J.S.; Langford, P.R.; Loynds, B.M.

J. Bacteriol. 173, 7449-7457, 1991

A;Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para

A;Reference number: A41654; MUID:92041655; PMID:1938942

A;Accession: D41654

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-4 <KRO>

Query Match 20.0%; Score 5; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 R 3

Db 2 R 2

RESULT 47

I40870

phospholipase C (BC 3.1.4.3) - Clostridium perfringens (fragment)

C;Species: Clostridium perfringens

C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000

C;Accession: I40870

R;Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.

Microbiol. Immunol. 36, 603-613, 1992

A;Title: Role of the upstream region containing an intrinsic DNA curvature in the negative

A;Reference number: I40870; MUID:92396045; PMID:1522810

A;Accession: I40870

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-4 <RES>

A;Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417

C;Genetics:

A;Gene: plc

C;Keywords: phosphoric diester hydrolase

Query Match 20.0%; Score 5; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 R 3

Db 3 R 3

RESULT 48

A35779

neuropeptide Antho-RNAmide - sea anemone (Anthopleura elegantissima)

C;Species: Anthopleura elegantissima

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 08-Dec-1995

C;Accession: A35779

R;Grimmelikhuijzen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; Nothmann

Proc. Natl. Acad. Sci. U.S.A. 87, 5410-5414, 1990

A;Title: Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNAmide), a sea anemone ne

A;Reference number: A35779; MUID:90319122; PMID:1973541

A;Accession: A35779

A;Molecule type: protein

A;Residues: 1-4 <GRI>

C;Comment: The L-3-phenyllactyl blocking group probably arises from an amino-terminal phe

C;Keywords: amidated carboxyl end; neuropeptide; phenyllactylation

F;1/Modified site: L-3-phenyllactic acid (Phe) #status experimental

F;4/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 20.0%; Score 5; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 R 3

Db 3 R 3

RESULT 49

A60418

FMRFamide - polychaete (Nereis virens)

C;Species: Nereis virens (sandworm)

C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 11-Jul-1997

C;Accession: A60418

R;Krajncak, K.G.; Price, D.A.

Peptides 11, 75-77, 1990

A;Title: Authentic FMRFamide is present in the polychaete Nereis virens.

A;Reference number: A60418; MUID:90259866; PMID:2342992

A;Accession: A60418

A;Molecule type: protein

A;Residues: 1-4 <KEA>

C;Keywords: amidated carboxyl end; neuropeptide

F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 5; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 R 3

Db 3 R 3

RESULT 50

I61883

protamine P1 - orangutan (fragment)

C;Species: Pongo pygmaeus (orangutan)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C;Accession: I61883

R;Queralt, R.; Oliva, R.

Gene 133, 197-204, 1993

A;Title: Identification of conserved potential regulatory sequences of the protamine-enc

A;Reference number: I37013; MUID:94040810; PMID:8224908

A;Accession: I61883

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372

Query Match 20.0%; Score 5; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 R 3

Db 3 R 3

Search completed: September 7, 2004, 19:25:39
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:21:52 ; Search time 9 Seconds
(without alignments)
23.142 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	12	48.0	4	1	TUFT HUMAN
2	7	28.0	3	1	THYL_PIG
3	7	28.0	4	1	DCML_PSECH
4	7	28.0	4	1	RWOL_YEAST
5	6	24.0	3	1	GRWM_HUMAN
6	6	24.0	4	1	ACH1_ACHFU
7	6	24.0	4	1	ACH1_HUMAN
8	6	24.0	4	1	OCPI_OCTMI
9	6	24.0	4	1	OCPI_OCTMI
10	5	20.0	4	1	PAR3_HIRME
11	5	20.0	4	1	PAR4_HIRME
12	5	20.0	4	1	FLRF_HIRME
13	5	20.0	4	1	FLRN_ANTEP
14	5	20.0	4	1	FWRF_MACNI
15	5	20.0	4	1	FYRI_ANTEP
16	2	8.0	3	1	LUXE_VIBET
17	2	8.0	4	1	DCMS_PSECH
18	2	8.0	4	1	FFKA_ANTEP

ALIGNMENTS

RESULT 1

ID TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=72187087; PubMed=4112769; Satoh P.S., Najjar V.A.;
RA Nishioka K., Constantopoulos A.,
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179 (1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392 (1967).
CC -I- MISCELLANEOUS: An IGG (called leucokinin) binds reversibly to the
cell membrane of neutrophils in the blood. Leucokininase on the
membrane releases the active peptide tuftsin from the gamma chain.
CC Tuftsin is essential for maximum stimulation of the phagocytic
activity of neutrophils.
DR PIR; A02147; A02147.
DR MIN; 191150; -.
DR GO; GO:0003823; Frantigen binding; NAS.
DR GO; GO:0006909; Phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 48.0%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PR 3

DB 3 PR 4

RESULT 2

ID THYL_PIG STANDARD; PRT; 3 AA.
AC P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
OS Sus scrofa (Pig).
OS Ovis aries (Sheep).
OS Bombina orientalis (Oriental fire-bellied toad), and
Notoptthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN NCBI_TaxID=9823, 9940, 8346, 8316;
RN [1]
RP SEQUENCE
RX SPECIES=Pig; TISSUE=Hypothalamus;
MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone.";
RL Biochemistry 9:1103-1106 (1970).
RN [2]
RP SYNTHESIS.
RX SPECIES=Pig;
MEDLINE=70039904; PubMed=4982117;
RA Boier J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
releasing hormone and pyroglutamyl-histidyl-proline amide.";
RL Biochem. Biophys. Res. Commun. 37:705-710 (1969).
RN [3]
RP SEQUENCE
RX SPECIES=Sheep; TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
RA Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid

RT stimulating hormone releasing factor of ovine origin by means of mass
RT spectrometry.";
RL Org. Mass Spectrom. 5:221-228(1971).
RN [4]

RP SYNTHESIS.
RC SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RT Guillemin R.;
RA "Characterization of ovine hypothalamic hypophysiotropic
RT TSH-releasing factor.";
RL Nature 226:321-325(1970).
RN [5]

RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RL Chem. Pharm. Bull. 23:3301-3303(1975).
RN [6]

RP SEQUENCE.
RC SPECIES=N.Viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "biosynthesis of thyrotropin releasing factor by newt (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor.";
RL J. Neurochem. 23:471-478(1974).
RN [7]

CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
in the anterior pituitary gland and as a neurotransmitter/
neuromodulator in the central and peripheral nervous systems.

DR PIR; A90819; RHTDIO.
DR PIR; A92971; A92971.
DR PIR; A93750; RSHST.
KW Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 3;
Best Local Similarity 100.0%; Pred.No.1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2
DB 3 P 3

RESULT 3
DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTL.

OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]

RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendick I., Hervig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydohydrogenic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.

CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; PLO140; PLO140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F000000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred.No.1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2
DB 4 P 4

RESULT 4
RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
GN MRPL1.

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]

RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.

DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D000000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred.No.1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2
DB 4 P 4

RESULT 5
GRAM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC growth of some cell types and to inhibit other types in vitro.

DR GO: GO:0001559; P: regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E8100000000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
DB 1 G 1

RESULT 6
ACH1 ACHFU
ID ACH1 ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Perussac; TISSUE=Ganglion;
EX MEDLINE=83273551; PubMed=2597281;
RA Kanatani Y., Minakata H., Kenny P. T. M., Iwashita T., Watanabe K.,
RA Funase K., Sun X. P., Yongsiri A., Kim K. H., Novales-Li P.,
RA Novales E. T., Kanapi C. G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
fulica Ferussac containing a D-amino acid residue";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Perussac; TISSUE=Heart atrium;
EX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I
D-amino acid residue";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
and produces a spike broadening of the identified heart excitatory
neuron (PON); also enhances the amplitude and frequency of the
heart beat. Has also an effect on several other muscles.
DR PIR; A32480; A32480.
FT MOD RES 2 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C81000000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
DB 1 G 1

RESULT 7
EOS1 HUMAN
ID EOS1_HUMAN STANDARD; PRT; 4 AA.

AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilotactic peptides.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E. J., Austen K. F.;
RT "Purification and synthesis of eosinophilotactic tetrapeptides of
human lung tissue: identification as eosinophil chemotactic factor of
anaphylaxis.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -!- MISCELLANEOUS: These peptides are released from mast cells in lung
(and other tissues) during hypersensitivity reactions
(anaphylaxis). Their activities, preferentially affecting
eosinophils, include chemotaxis, chemotactic deactivation, release
of enzymes, and stimulation of the hexose monophosphate shunt.
DR GO: GO:0006935; P: chemotaxis; IDA.
DR GO: GO:0006955; P: immune response; IDA.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT SEQUENCE 4 AA; 390 MW; 6B05B862A000000000 CRC64;
/FTID=VAR 005201.

Query Match 24.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
DB 2 G 2

RESULT 8
OCPI OCTMI
ID OCPI OCTMI STANDARD; PRT; 4 AA.
AC P58638;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardiacactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89786;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-2 is a 1000 time less
active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=NALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-PHENYLALANINE (IN OCP-1).
SQ SEQUENCE 4 AA; 394 MW; 6AA879C81000000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1

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Db      1 G 1
RESULT 9
OCP3_OCTMI
ID_OCP3_OCTMI  STANDARD;      PRT;      4 AA.
AC  P36649;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Cardioactive peptides Ocp-3/Ocp-4.
OS  Octopus minor (Octopus).
OC  Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC  Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX  NCBI_TaxID=89766;
RN  [1]
RP  SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC  TISSUE=Brain;
RX  MEDLINE=20336815; PubMed=10876044;
RA  Iwakashi E., Hisada M., Minakata H.;
RT  "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT  Octopus minor.";
RL  Peptides 21:623-630(2000).
CC  -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC  inotropic effects on the heart. Ocp-4 is a 1000 time less
CC  active than Ocp-3.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- FM: Ocp-4 has D-Ser instead of L-Ser.
CC  -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW  Hormone; D-amino acid.
FT  MOD RES 2 2 D-SERINE (IN OCP-4).
SQ  SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 G 1
Db      1 G 1

RESULT 10
FAR3_HIRME
ID_FAR3_HIRME  STANDARD;      PRT;      4 AA.
AC  P42562;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  FMRamide-like neuropeptide YLRF-amide.
OS  Hirudo medicinalis (Medicinal leech).
OC  Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC  Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX  NCBI_TaxID=6421;
RN  [1]
RP  SEQUENCE.
RX  SPECIES=H. medicinalis;
RX  MEDLINE=92195954; PubMed=1686933;
RA  Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT  "Identification of Rfamide neuropeptides in the medicinal leech.";
RL  Peptides 12:897-908(1991).
CC  -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC  family.
KW  Neuropeptide; Amidation.
FT  MOD RES 4 4 AMIDATION.
SQ  SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  3 R 3
Db      3 R 3

RESULT 11
FAR4_HIRME
ID_FAR4_HIRME  STANDARD;      PRT;      4 AA.
AC  P42563;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  FMRamide-like neuropeptide YMRF-amide.
OS  Hirudo medicinalis (Medicinal leech).
OC  Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC  Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX  NCBI_TaxID=6421;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=92195954; PubMed=1686933;
RA  Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT  "Identification of Rfamide neuropeptides in the medicinal leech.";
RL  Peptides 12:897-908(1991).
CC  -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC  family.
KW  Neuropeptide; Amidation.
FT  MOD RES 4 4 AMIDATION.
SQ  SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  3 R 3
Db      3 R 3

RESULT 12
FLRF_HIRME
ID_FLRF_HIRME  STANDARD;      PRT;      4 AA.
AC  P42561;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  FLRFamide.
OS  Hirudo medicinalis (Medicinal leech), and
OS  Helisoma trivolvis (Snail).
OC  Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC  Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX  NCBI_TaxID=6421, 27815;
RN  [1]
RP  SEQUENCE.
RX  SPECIES=H. medicinalis;
RX  MEDLINE=92195954; PubMed=1686933;
RA  Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT  "Identification of Rfamide neuropeptides in the medicinal leech.";
RL  Peptides 12:897-908(1991).
RN  [2]
RP  SEQUENCE.
RX  SPECIES=H. trivolvis; TISSUE=Kidney;
RX  MEDLINE=94286417; PubMed=7912428;
RA  Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT  "FMRamide-related peptides from the kidney of the snail, Helisoma
RT  trivolvis.";
RL  Peptides 15:31-36(1994).
CC  -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC  family.
KW  Neuropeptide; Amidation.
FT  MOD RES 4 4 AMIDATION.
SQ  SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  3 R 3
Db      3 R 3

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Qy 3 R 3
Db 3 R 3

RESULT 13

FLRN ANTEL STANDARD; PRT; 4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheld R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAE.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD RES 1 1 L-3-PHENYLLACTYL.
FT MOD RES 4 1 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
Db 3 R 3

RESULT 14

FWRF MACNI STANDARD; PRT; 4 AA.
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocallista nimbosa (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Veneroidea; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
[1]
RN SEQUENCE, AND SYNTHESIS.
RP SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and visceral ganglion;
RX MEDLINE=77215956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671 (1977).
[2]
RN SEQUENCE, AND CHARACTERIZATION
RP SPECIES=M.nimbosa; TISSUE=ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
from the central ganglia of a bivalve mollusc.";

RL Prep. Biochem. 7:261-281 (1977).
RN [3]
RP SEQUENCE.
RC SPECIES=N.virens;
RX MEDLINE=90259866; PubMed=2342992;
RA Krajciak K.G., Price D.A.;
RT "Authentic FMRamide is present in the polychaete Nereis virens.";
RL Peptides 11:75-77 (1990).
[4]
RN SEQUENCE.
RP SPECIES=H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-906 (1991).
[5]
RN SEQUENCE.
RP SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
trivolvis";
RL Peptides 13:31-36 (1994).
CC -1- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
activities include augmentation, induction, and regulation of
cardiac contraction.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; A01426; ECKK
DR PIR; A60418; A60418.
KW Neuropeptide; Amidation.
FT MOD RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
Db 3 R 3

RESULT 15

FYRI ANTEL STANDARD; PRT; 4 AA.
AC P58706;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antho-RNamide I [Contains: Antho-RNamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
[1]
RN SEQUENCE
RP MEDLINE=92270459; PubMed=1821096;
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its
des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173 (1991).
[2]
RN FUNCTION.
RP MEDLINE=93391436; PubMed=8397415;
RX McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-Kamide and Antho-RNamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188 (1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding

CC behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SPECIFICITY: Neuron specific.
 KW Neuropeptide; Amidation.
 FT CHAIN 1 4 ANTHO-RIAMIDE I.
 FT CHAIN 2 4 ANTHO-RIAMIDE II.
 FT MOD_RES 1 1 L-3-PHENYLACTYL.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
 Db 3 R 3

RESULT 16
 LUXE_VIBFI STANDARD; PRT; 3 AA.
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
 DE protein synthetase) (Fragment).
 GN LUXE.
 OS Vibrio fischeri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=568;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91072226; PubMed=2254256;
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
 RT site for the lux operon."
 RL J. Bacteriol. 172:6797-6802(1990).
 CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
 CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
 CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
 CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M2812; ; NOT ANNOTATED_CDS.
 DR Luminescence; Ligase.
 KW NON TER 1 1
 FT MOD_RES 1 1
 SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 8.0%; Score 2; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
 Db 2 K 2

RESULT 17
 DCMS_PSECH STANDARD; PRT; 4 AA.
 ID DCMS_PSECH

AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydophilic bacteria."
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: Binds 2 2Fe-2S clusters.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 CC PIR: P10146; P10146.
 KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 8.0%; Score 2; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
 Db 3 K 3

RESULT 18
 PFKA_ANTEL STANDARD; PRT; 4 AA.
 ID PFKA_ANTEL
 AC P58705;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-KAamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nyantheae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92028852; PubMed=1691803;
 RA Nethacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
 RT "Isolation of l-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
 RT novel neuropeptide from sea anemones."
 RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nethacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 RT inhibitory neuropeptides, Antho-KAamide and Antho-KRAMide."
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron specific.
 DR PIR; JQ1273; JQ1273.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 SQ SEQUENCE 1 1 L-3-PHENYLACTYL.

FT MOD RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339CA00000000 CRC64;

Query Match 8.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 R 3
Db 3 K 3

Search completed: September 7, 2004, 19:24:35
Job time : 9 secs

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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:22:11 ; Search time 36 Seconds
(without alignments)
35.058 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organalle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	24.0	2	5 P83570	P83570 sepi offic
2	2	8.0	4	11 Q08433	Q08433 rattus sp.
3	0	0.0	4	5 P83568	P83568 sepi offic

ALIGNMENTS

RESULT 1

ID P83570 PRELIMINARY; PRT; 2 AA.
AC P83570;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Neuropeptide Gwa.

OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX PubMed=9437704;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Tyr-amide-related peptide inhibiting the motility of the mature oviduct in the cuttlefish, Sepia officinalis";
RL Peptides 18:1459-1474(1997).
CC -|- FUNCTION: REGULATORY NEUROPEPTIDE WITH MYOTROPIC ACTIVITY TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT BY DECREASING TONUS, FREQUENCY AND AMPLITUDE OF CONTRACTIONS.
CC -|- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.
CG GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD RES 2 2 AMIDATION
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 24.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1

Db 1 G 1

RESULT 2

ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aoto S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON TER 1 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 8.0%; Score 2; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 1e+06;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3

Db 4 K 4

RESULT 3

ID P83568 PRELIMINARY; PRT; 4 AA.
AC P83568;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Neuropeptide Gwa.

DE Pheromone peptide ILME.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=EGG;
 RX PubMed=10944467;
 RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
 RT "ILME, a waterborne pheromonal peptide released by the eggs of Sepia
 RT officinalis."; Biochem. Biophys. Res. Commun. 275:217-222(2000).
 RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=EGG;
 RX PubMed=12207899;
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 RT attracting peptide."; Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
 CC -|- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
 CC -|- SUBCELLULAR LOCATION: SECRETED.
 CC -|- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG(EC2).
 CC -|- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
 DR GO; GO:0005186; F:pheromone activity; IEA.
 KW Pheromone.
 SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 0.0%; Score 0; DB 5; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 R 3
 Db 4 E 4

Search completed: September 7, 2004, 19:25:17
 Job time : 36 secs

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OM protein : protein search, using sw model

Run on: September 7, 2004, 18:58:28 ; Search time 416 Seconds
(without alignments)

9.385 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Pending Patents 1A Main.*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
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- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US099A_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
- 28: /cgn2_6/ptodata/2/paa/US103_COMB.pep.*
- 29: /cgn2_6/ptodata/2/paa/US104_COMB.pep.*
- 30: /cgn2_6/ptodata/2/paa/US105_COMB.pep.*
- 31: /cgn2_6/ptodata/2/paa/US106_COMB.pep.*
- 32: /cgn2_6/ptodata/2/paa/US107_COMB.pep.*
- 33: /cgn2_6/ptodata/2/paa/US108_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	25	100.0	4	1	PCT-US03-07665-1	Sequence 1, Appli
2	25	100.0	4	1	PCT-US03-24864-1	Sequence 1, Appli
3	25	100.0	4	1	PCT-US03-30112-1	Sequence 1, Appli
4	25	100.0	4	1	PCT-US98-27660-6	Sequence 6, Appli
5	25	100.0	4	1	PCT-US98-27660-6	Sequence 6, Appli
6	25	100.0	4	3	US-07-705-071-5	Sequence 5, Appli
7	25	100.0	4	5	US-08-138-820-4	Sequence 4, Appli
8	25	100.0	4	6	US-08-260-514-4	Sequence 4, Appli
9	25	100.0	4	11	US-08-753-781B-2	Sequence 2, Appli
10	25	100.0	4	13	US-08-982-981-1	Sequence 1, Appli
11	25	100.0	4	14	US-09-040-712-3	Sequence 3, Appli
12	25	100.0	4	14	US-09-091-578B-5	Sequence 5, Appli
13	25	100.0	4	16	US-09-218-660-4	Sequence 4, Appli
14	25	100.0	4	17	US-09-376-529-2	Sequence 2, Appli
15	25	100.0	4	19	US-09-593-117-6	Sequence 6, Appli
16	25	100.0	4	20	US-09-639-634A-4	Sequence 4, Appli
17	25	100.0	4	20	US-09-687-156A-1	Sequence 1, Appli
18	25	100.0	4	20	US-09-699-679A-4	Sequence 4, Appli
19	25	100.0	4	22	US-09-763-777B-2	Sequence 2, Appli
20	25	100.0	4	22	US-09-779-054-16	Sequence 16, Appli
21	25	100.0	4	23	US-09-813-484-6	Sequence 6, Appli
22	25	100.0	4	24	US-09-931-009A-2	Sequence 2, Appli
23	25	100.0	4	26	US-10-016-569A-25	Sequence 25, Appli
24	25	100.0	4	26	US-10-046-801-5	Sequence 6, Appli
25	25	100.0	4	29	US-10-308-644-25	Sequence 25, Appli
26	25	100.0	4	31	US-10-674-756-9	Sequence 9, Appli
27	25	100.0	5	4	US-08-085-126-76	Sequence 76, Appli
28	25	100.0	5	8	US-08-438-114-76	Sequence 76, Appli
29	25	100.0	5	17	US-09-376-529-3	Sequence 3, Appli
30	25	100.0	5	18	US-09-462-446A-1	Sequence 1, Appli
31	25	100.0	5	18	US-09-462-446A-2	Sequence 2, Appli
32	25	100.0	5	22	US-09-763-777B-3	Sequence 3, Appli
33	25	100.0	5	25	US-09-953-657-4	GENERAL INFORMA
34	25	100.0	5	31	US-10-619-520-1	Sequence 1, Appli
35	25	100.0	5	31	PCT-US03-11798-28	Sequence 28, Appli
36	25	100.0	6	1	PCT-US03-11799-23	Sequence 23, Appli
37	25	100.0	6	30	US-10-414-523-23	Sequence 23, Appli
38	25	100.0	6	30	US-10-414-524-28	Sequence 28, Appli
39	25	100.0	7	1	PCT-US03-17245-14	Sequence 14, Appli
40	25	100.0	7	20	US-09-687-156A-3	Sequence 3, Appli
41	25	100.0	7	20	US-09-687-156A-4	Sequence 4, Appli
42	25	100.0	7	20	US-09-687-156A-5	Sequence 5, Appli
43	25	100.0	7	20	US-09-687-156A-6	Sequence 6, Appli
44	25	100.0	7	20	US-09-687-156A-7	Sequence 7, Appli
45	25	100.0	7	20	US-09-687-156A-8	Sequence 8, Appli
46	25	100.0	7	20	US-09-687-156A-9	Sequence 9, Appli
47	25	100.0	7	20	US-09-687-156A-10	Sequence 10, Appli
48	25	100.0	7	20	US-09-687-156A-11	Sequence 11, Appli
49	25	100.0	7	20	US-09-687-156A-12	Sequence 12, Appli
50	25	100.0	7	20	US-09-687-156A-13	Sequence 13, Appli
51	25	100.0	7	20	US-09-687-156A-14	Sequence 14, Appli
52	25	100.0	7	30	US-08-449-659-14	Sequence 14, Appli
53	25	100.0	8	4	US-08-085-126-79	Sequence 79, Appli
54	25	100.0	8	8	US-08-438-114-79	Sequence 79, Appli
55	25	100.0	8	8	US-08-478-725-33	Sequence 33, Appli
56	25	100.0	8	19	US-09-566-047-105	Sequence 105, App
57	25	100.0	8	20	US-09-687-156A-45	Sequence 45, Appli
58	25	100.0	8	20	US-09-687-156A-46	Sequence 46, Appli
59	25	100.0	8	32	US-10-742-079-105	Sequence 105, App
60	25	100.0	9	1	PCT-US03-24488-49	Sequence 49, Appli
61	25	100.0	9	1	PCT-US03-24488-117	Sequence 117, App
62	25	100.0	9	18	US-09-455-613-3	Sequence 3, Appli
63	25	100.0	9	18	US-09-455-613A-3	Sequence 3, Appli
64	25	100.0	9	18	US-09-462-446A-8	Sequence 8, Appli
65	25	100.0	9	18		

ALIGNMENTS

RESULT 1
PCT-US03-07665-1
; Sequence 1, Application PC/TUS0307665

; GENERAL INFORMATION:
 ; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
 ; APPLICANT: BRESAGEN LIMITED
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRIMATE NEURAL CELL
 ; TITLE OF INVENTION: PRODUCTION
 ; FILE REFERENCE: 18465-0023
 ; CURRENT APPLICATION NUMBER: PCT/US03/07665
 ; CURRENT FILING DATE: 2003-03-13
 ; PRIOR APPLICATION NUMBER: 60/364,381
 ; PRIOR FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 PCT-US03-07665-1

Query Match 100.0%; Score 25; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 2
 PCT-US03-24864-1
 ; GENERAL INFORMATION:
 ; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
 ; APPLICANT: BRESAGEN, LTD.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL DIFFERENTIATION
 ; TITLE OF INVENTION: OF EMBRYONIC STEM CELLS
 ; FILE REFERENCE: 18465-0024
 ; CURRENT APPLICATION NUMBER: PCT/US03/24864
 ; CURRENT FILING DATE: 2003-08-08
 ; PRIOR APPLICATION NUMBER: US 60/401,968
 ; PRIOR FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: US 60/459,090
 ; PRIOR FILING DATE: 2003-03-31
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 PCT-US03-24864-1

Query Match 100.0%; Score 25; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 3
 PCT-US03-30112-1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRESAGEN, LTD.
 ; APPLICANT: MEDICAL COLLEGE OF GEORGIA RESEARCH INSTITUTE
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENRICHMENT OF NEURAL STEM
 ; TITLE OF INVENTION: CELLS USING CERAMIDE ANALOGS

; FILE REFERENCE: 18377-0024
 ; CURRENT APPLICATION NUMBER: PCT/US03/30112
 ; CURRENT FILING DATE: 2003-09-25
 ; PRIOR APPLICATION NUMBER: US 60/413,510
 ; PRIOR FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 60/485,351
 ; PRIOR FILING DATE: 2003-07-07
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 PCT-US03-30112-1

Query Match 100.0%; Score 25; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 4
 PCT-US98-27060-6
 ; Sequence 6, Application PC/TUS9827060
 ; GENERAL INFORMATION:
 ; APPLICANT: IMARX PHARMACEUTICAL CORP.
 ; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
 ; FILE REFERENCE: UNGR-1536
 ; CURRENT APPLICATION NUMBER: PCT/US98/27060
 ; CURRENT FILING DATE: 1998-12-17
 ; EARLIER APPLICATION NUMBER: 08/993,165
 ; EARLIER FILING DATE: 1997-12-18
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: novel sequence
 PCT-US98-27060-6

Query Match 100.0%; Score 25; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
 Db 1 GPRP 4

RESULT 5
 PCT-US98-27060-6
 ; Sequence 6, Application PC/TUS9827060A
 ; GENERAL INFORMATION:
 ; APPLICANT: IMARX PHARMACEUTICAL
 ; TITLE OF INVENTION: Optacoustic
 ; FILE REFERENCE: UNGR1536
 ; CURRENT APPLICATION NUMBER: PCT/US98/27060A
 ; CURRENT FILING DATE: 1998-12-17
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence

PCT-US98-27060-6

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 6

US-07-705-071-5
Sequence 5, Application US/07705071
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07705,071
FILING DATE: 19910524
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-07-705-071-5
Query Match 100.0%; Score 25; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 7

US-08-138-820-4
Sequence 4, Application US/08138820
GENERAL INFORMATION:
APPLICANT: Klein, Scott I.
TITLE OF INVENTION: ANTITHROMBOTIC AZACYCLOALKYLKANOLYL
PEPTIDES AND PSEUDOPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43

CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (Patent In)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,820
FILING DATE: 15-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Darks, Paul R.
REGISTRATION/DOCKET NUMBER: 33,862
REFERENCE/DOCKET NUMBER: A1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3820
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-138-820-4
Query Match 100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
DB 1 GPRP 4

RESULT 8

US-08-260-514-4
Sequence 4, Application US/08260514
GENERAL INFORMATION:
APPLICANT: Muir, Thomas W.
TITLE OF INVENTION: Structural Models for Cytoplasmic
Domains of Transmembrane Receptors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,514
FILING DATE: 15-JUN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B.
REGISTRATION/DOCKET NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 30457.6-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 445-1140
TELEFAX: (310) 445-9031

```

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Ligand sequence recognized by integrin
;
US-08-260-514-4
Query Match 100.0%; Score 25; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 9
US-08-753-781B-2
; Sequence 2, Application US/08753781B
; GENERAL INFORMATION:
; APPLICANT: Markland, Francis S
; APPLICANT: Bush, Larry R
; APPLICANT: Swenson, Stephen
; APPLICANT: Sanchez, Bladio F
; TITLE OF INVENTION: Thrombolytic Agents with Antithrombotic
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,781B
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,2056
; TELEPHONE: 312 913 0001
; TELEFAX: 312 913 0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-753-781B-2
Query Match 100.0%; Score 25; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 10
US-08-982-981-1
; Sequence 1, Application US/08982981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Bladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/982,981
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/753,781
; FILING DATE: 02-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 124.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 603 437 8970
; TELEFAX: 603 437 8977
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-982-981-1
Query Match 100.0%; Score 25; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 11
US-09-040-712-3
; Sequence 3, Application US/09040712
; GENERAL INFORMATION:
; APPLICANT: Durbin, Dennis A.
; APPLICANT: Lee, Theodore T.
; APPLICANT: Ratnikov, Boris I.
; APPLICANT: Hillman, Robert S.
; APPLICANT: Smith, Jeffrey W.
; TITLE OF INVENTION: AGGLUTINIMETRIC ASSAYS IN BLOOD
; FILE REFERENCE: 22608-0014P1
; CURRENT APPLICATION NUMBER: US/09/040,712
; CURRENT FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: US 08/820,999
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3

```

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; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GRRP Peptide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Peptide inhibitor of fibrin polymerization.
US-09-040-712-3

Query Match      100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 1 GRRP 4

RESULT 12
US-09-091-578B-5
; Sequence 5, Application US/09091578B
; GENERAL INFORMATION:
; APPLICANT: MADISON, EDWIN L.
; TITLE OF INVENTION: TARGETED THERAPEUTIC OR DIAGNOSTIC
; FILE REFERENCE: 19191.0002
; CURRENT APPLICATION NUMBER: US/09/091.578B
; CURRENT FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PCT/US96/20577
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: 60/005,028
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: artificial construct
US-09-091-578B-5

Query Match      100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 1 GRRP 4

RESULT 13
US-09-218-660-4
; Sequence 4, Application US/09218660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Shen, Dekang
; APPLICANT: Wu, Guanli
; TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And
; FILE REFERENCE: DUP-0307
; CURRENT APPLICATION NUMBER: US/09/218,660
; CURRENT FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 08/660,032
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 08/640,464
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/497,684
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-218-660-4

Query Match      100.0%; Score 25; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 1 GRRP 4

RESULT 14
US-09-376-529-2
; Sequence 2, Application US/09376529
; GENERAL INFORMATION:
; APPLICANT: Thakur, Madhukar L.
; TITLE OF INVENTION: Imaging With TC-99 Labeled
; FILE REFERENCE: THA01.NP003
; CURRENT APPLICATION NUMBER: US/09/376,529
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/096,803
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown
US-09-376-529-2

Query Match      100.0%; Score 25; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 1 GRRP 4

RESULT 15
US-09-593-117-6
; Sequence 6, Application US/09593117
; GENERAL INFORMATION:
; APPLICANT: Wu, Yungliu
; APPLICANT: Evan C., Unger
; TITLE OF INVENTION: Optoacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1594
; CURRENT APPLICATION NUMBER: US/09/593,117
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 08/993,165
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-593-117-6

Query Match      100.0%; Score 25; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|
|
|
|
Db 1 GPRP 4

RESULT 16

US-09-639-634A-4
; Sequence 4, Application US/09639634A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Chrzap, Zofia J
; APPLICANT: Mancel, James J
; APPLICANT: Toledo-Valasquez, David
; APPLICANT: Windisch, Vincent
; APPLICANT: Woodward, Rick G.
; APPLICANT: Salazar, Diane (Deceased) C
; APPLICANT: Salazar, Richard (Legal Representative) C
; APPLICANT: Venuri, Narasimha M
; APPLICANT: Gardetto, Anthony J.
; APPLICANT: Matthew, Powers R.
; APPLICANT: Kubiak, Gregory G.
; APPLICANT: Liu, Robert C.
; APPLICANT: Vanasse, Benoit J.
; APPLICANT: Sherbine, James P.
; APPLICANT: Rodriguez, Walter
; APPLICANT: Slideski, Adam W.
; TITLE OF INVENTION: STABLE NON-HYDROSCOPIC CRYSTALLINE FORM OF N-[N-(4-(PIPERIDIN-1-YL)BUTANOYL)-N-ETHYLGLYCYL]ASPARTYL-L-BETA-CYCLOHEXYL ALANINE A
; TITLE OF INVENTION: INTERMEDIATES THEREOF, AND PREPARATION THEREOF AND OF ANTITHROMB
; TITLE OF INVENTION: AZACYCLOALKYLALKANOYL PEPTIDES AND PSEUDOPEPTIDES
; FILE REFERENCE: A2234B US
; CURRENT APPLICATION NUMBER: US/09/639,634A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 09/251,030
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: PCT/US97/14756
; PRIOR FILING DATE: 1997-08-21
; PRIOR APPLICATION NUMBER: 60/024,284
; PRIOR FILING DATE: 1996-08-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide capable of inhibiting binding of fibrinogen to platelets
; OTHER INFORMATION: platelets

US-09-639-634A-4

Query Match 100.0%; Score 25; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|
|
|
|
Db 1 GPRP 4

RESULT 17

US-09-687-156A-1
; Sequence 1, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; APPLICANT: Messmer, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; TITLE OF INVENTION: MIXTURES
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

US-09-687-156A-1

Query Match 100.0%; Score 25; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|
|
|
|
Db 1 GPRP 4

RESULT 18

US-09-699-679A-4
; Sequence 4, Application US/09699679A
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, Dekang
; APPLICANT: Wu, Guanli
; TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And Therapeutic Use
; FILE REFERENCE: UNGR1598
; CURRENT APPLICATION NUMBER: US/09/699,679A
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/218,660
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 08/660,032
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 08/640,464
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/497,684
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct

US-09-699-679A-4

Query Match 100.0%; Score 25; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|
|
|
|
Db 1 GPRP 4

RESULT 19

US-09-763-777B-2
; Sequence 2, Application US/09763777B
; GENERAL INFORMATION:
; APPLICANT: Thakur, Madhukar (Matthew) L.
; TITLE OF INVENTION: Imaging with TC-99m Labeled Fibrin Alpha Peptide
; TITLE OF INVENTION: Chain Peptide
; FILE REFERENCE: 8321-119
; CURRENT APPLICATION NUMBER: US/09/763,777B
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/19011
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,803
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2


```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of N-terminus tripeptide identified in SEQ
; OTHER INFORMATION: ID NO: 1
US-09-763-777B-2

Query Match      100.0%; Score 25; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 20
US-09-779-054-16
; Sequence 16, Application US/09779054
; GENERAL INFORMATION:
; APPLICANT: Lu, Xinjie
; APPLICANT: Kakkar, Vijay
; TITLE OF INVENTION: USE OF DENDROASPIN AS A SCAFFOLD FOR NON-DENDROASPIN DOMAINS
; FILE REFERENCE: A-70312/TAL/AMS
; CURRENT APPLICATION NUMBER: US/09/779,054
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: GB 0002625.2
; PRIOR FILING DATE: 2000-02-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: thrombin-binding sequence
US-09-779-054-16

Query Match      100.0%; Score 25; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 21
US-09-813-484-6
; Sequence 6, Application US/09813484
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Precu
; FILE REFERENCE: UNGR1600
; CURRENT APPLICATION NUMBER: US/09/813,484
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/929,847
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-09-813-484-6

Query Match      100.0%; Score 25; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 22
US-09-931-009A-2
; Sequence 2, Application US/09931009A
; GENERAL INFORMATION:
; APPLICANT: Smith, Theresa H.
; TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
; FILE REFERENCE: US 1257/01 (VA)
; CURRENT APPLICATION NUMBER: US/09/931,009A
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown. Obtained from a commercial source.
US-09-931-009A-2

Query Match      100.0%; Score 25; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 23
US-10-016-569A-25
; Sequence 25, Application US/10016569A
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ling-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kae-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: P1379
; CURRENT APPLICATION NUMBER: US/10/016,569A
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
US-10-016-569A-25

Query Match      100.0%; Score 25; DB 26; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 24
US-10-046-801-6
; Sequence 6, Application US/10046801
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
```

```
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-10-046-801-6

Query Match          100.0%; Score 25; DB 26; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
Db      1 GPRP 4

RESULT 25
US-10-308-644-25
; SEQUENCE 25, Application US/10308644
; GENERAL INFORMATION:
; APPLICANT: Wu, Shih-Kwang
; APPLICANT: Tseng, Chin-Lu
; APPLICANT: Chang, Ting-Gung
; APPLICANT: Chen, Li-Jung
; APPLICANT: Shih, Kea-Shyang
; TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
; TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
; FILE REFERENCE: P1379
; CURRENT APPLICATION NUMBER: US/10/308,644
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human Cell
US-10-308-644-25

Query Match          100.0%; Score 25; DB 29; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
Db      1 GPRP 4

RESULT 26
US-10-674-756-9
; SEQUENCE 9, Application US/10674756
; GENERAL INFORMATION:
; APPLICANT: FORWOOD, JADE KENNETH
; APPLICANT: MORRIS, MICHAEL BRADLEY
; TITLE OF INVENTION: RECEPTOR EXPRESSED IN PLURIPOTENT CELLS
; FILE REFERENCE: 18377-0025
; CURRENT APPLICATION NUMBER: US/10/674,756
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: AU 2002952398
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-674-756-9

Query Match          100.0%; Score 25; DB 31; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
Db      1 GPRP 4

RESULT 27
US-08-085-126-76
; SEQUENCE 76, Application US/08085126
; GENERAL INFORMATION:
; APPLICANT: LADNER, Robert C.
; APPLICANT: CANNON, Larick E.
; TITLE OF INVENTION: CHELYDRYZYMES AND NEPAZYMES, AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 236
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,126
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LADNER=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-085-126-76

Query Match          100.0%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
Db      1 GPRP 4

RESULT 28
US-08-438-114-76
; SEQUENCE 76, Application US/08438114
; GENERAL INFORMATION:
; APPLICANT: LADNER, Richard C.
; APPLICANT: CANNON, Larick E.
; TITLE OF INVENTION: CHELYDRYZYMES AND NEPAZYMES, AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 240
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,114
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,793
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/085,126
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LADNER-108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-438-114-76

Query Match 100.0%; Score 25; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 29
US-09-376-529-3
; Sequence 3, Application US/09376529
; GENERAL INFORMATION:
; APPLICANT: Thakur, Madhukar L.
; TITLE OF INVENTION: Imaging With TC-99 Labeled
; FILE OF INVENTION: Fibrin-Alpha-Chain Peptide
; FILE REFERENCE: THA01.NP003
; CURRENT APPLICATION NUMBER: US/09/376,529
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/096,803
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 4.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown
US-09-376-529-3

Query Match 100.0%; Score 25; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 30
US-09-462-446A-1
; Sequence 1, Application US/09462446A
; GENERAL INFORMATION:
; APPLICANT: Robert, Koll
; APPLICANT: Richter, W.
; APPLICANT: Bieber, Franz
; APPLICANT: Tschoppe, W.
; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
; FILE REFERENCE: Attorney Docket No. 1328/2
; CURRENT APPLICATION NUMBER: US/09/462,446A
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Synthesized Peptide
US-09-462-446A-1

Query Match 100.0%; Score 25; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 31
US-09-462-446A-2
; Sequence 2, Application US/09462446A
; GENERAL INFORMATION:
; APPLICANT: Robert, Koll
; APPLICANT: Richter, W.
; APPLICANT: Bieber, Franz
; APPLICANT: Tschoppe, W.
; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
; FILE REFERENCE: Attorney Docket No. 1328/2
; CURRENT APPLICATION NUMBER: US/09/462,446A
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Synthesized Peptide
US-09-462-446A-2

Query Match 100.0%; Score 25; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

		TELEFAX: (510)705-7904
		JOURNAL: Thromb. Haemost.
		VOLUME: 63
		ISSUE: 3
		PAGES: 439-444
		DATE: 28-JUN-1990
		SEQUENCE DESCRIPTION: SEQ ID NO: 4;
		US-09-953-657-4
		Query Match 100.0%; Score 25; DB 25; Length 5;
		Best Local Similarity 100.0%; Pred. No. 5.5e+06;
		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GRP 4	
Dd	1 GRP 4	
		RESULT 34
		US-10-619-520-1
		; Sequence 1, Application US/10619520
		; GENERAL INFORMATION:
		; APPLICANT: Robert, Koll
		; APPLICANT: Richter, W.
		; APPLICANT: Bieber, Franz
		; APPLICANT: Tschoppe, W.
		; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS-
		; FILE REFERENCE: Attorney Docket No. 1328/2
		; CURRENT APPLICATION NUMBER: US/10/619,520
		; CURRENT FILING DATE: 2003-07-14
		; NUMBER OF SEQ ID NOS: 8
		; SOFTWARE: Patentin version 3.0
		; SEQ ID NO 1
		; LENGTH: 5
		; TYPE: PRT
		; ORGANISM: Artificial Sequence
		; FEATURE:
		; NAME/KEY: PEPTIDE
		; LOCATION: (1)..(5)
		; OTHER INFORMATION: X is any amino acid
		; FEATURE:
		; NAME/KEY: PEPTIDE
		; LOCATION: (1)..(5)
		; OTHER INFORMATION: Synthesized Peptide
		US-10-619-520-1
		Query Match 100.0%; Score 25; DB 31; Length 5;
		Best Local Similarity 100.0%; Pred. No. 5.5e+06;
		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GRP 4	
Dd	1 GRP 4	
		RESULT 35
		US-10-619-520-2
		; Sequence 2, Application US/10619520
		; GENERAL INFORMATION:
		; APPLICANT: Robert, Koll
		; APPLICANT: Richter, W.
		; APPLICANT: Bieber, Franz
		; APPLICANT: Tschoppe, W.
		; TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS-
		; FILE REFERENCE: Attorney Docket No. 1328/2
		; CURRENT APPLICATION NUMBER: US/10/619,520
		; CURRENT FILING DATE: 2003-07-14
		; NUMBER OF SEQ ID NOS: 8
		; SOFTWARE: Patentin version 3.0
		; SEQ ID NO 2
		; LENGTH: 5
		; TYPE: PRT
		; ORGANISM: Artificial Sequence

```
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Synthesized Peptide
US-10-619-520-2

Query Match
Best Local Similarity 100.0%; Score 25; DB 31; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 36
PCT-US03-11798-28
; Sequence 28, Application PC/TUS0311798
; GENERAL INFORMATION:
; APPLICANT: American National Red Cross
; TITLE OF INVENTION: PLASMA PROTEIN-BINDING LIGANDS
; FILE REFERENCE: 221947
; CURRENT APPLICATION NUMBER: PCT/US03/11798
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,091
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US03-11798-28

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 37
PCT-US03-11799-23
; Sequence 23, Application PC/TUS0311799
; GENERAL INFORMATION:
; APPLICANT: American National Red Cross
; TITLE OF INVENTION: METHOD FOR DETECTING LIGANDS AND TARGETS IN A MIXTURE
; FILE REFERENCE: 221007
; CURRENT APPLICATION NUMBER: PCT/US03/11799
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/372,091
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US03-11799-23

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 38
US-10-414-523-23
; Sequence 23, Application US/10414523
; GENERAL INFORMATION:
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD FOR DETECTING LIGANDS AND TARGETS IN A MIXTURE
; FILE REFERENCE: 221429
; CURRENT APPLICATION NUMBER: US/10/414,523
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/372,091
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-414-523-23

Query Match
Best Local Similarity 100.0%; Score 25; DB 30; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 39
US-10-414-524-28
; Sequence 28, Application US/10414524
; GENERAL INFORMATION:
; APPLICANT: Hammond et al.
; TITLE OF INVENTION: PLASMA PROTEIN-BINDING LIGANDS
; FILE REFERENCE: 221948
; CURRENT APPLICATION NUMBER: US/10/414,524
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,091
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-414-524-28

Query Match
Best Local Similarity 100.0%; Score 25; DB 30; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
Db 1 GPRP 4

RESULT 40
PCT-US03-17245-14
; Sequence 14, Application PC/TUS0317245
; GENERAL INFORMATION:
; APPLICANT: Cognosci, Inc.
; APPLICANT: Moss, Marcia Lynn
; APPLICANT: Rasmussen, Fred H.
; APPLICANT: Vitek, Michael P.
```

```
; TITLE OF INVENTION: Assays for measuring matrix metalloproteinase activities
; FILE REFERENCE: 56816-5001-WO
; CURRENT APPLICATION NUMBER: PCT/US03/17245
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/384,135
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: metalloproteinase substrate
PCT-US03-17245-14

Query Match      100.0%; Score 25; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 41
US-09-687-156A-3
; Sequence 3, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; APPLICANT: Messmer, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-3

Query Match      100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 42
US-09-687-156A-4
; Sequence 4, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; APPLICANT: Messmer, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-4

Query Match      100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 43
US-09-687-156A-5
; Sequence 5, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; APPLICANT: Messmer, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-5

Query Match      100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 44
US-09-687-156A-6
; Sequence 6, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; APPLICANT: Messmer, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-6

Query Match      100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 45
US-09-687-156A-6
; Sequence 6, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; APPLICANT: Messmer, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-6

Query Match      100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4
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US-09-687-156A-7
; Sequence 7, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-7
Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-8
; Sequence 8, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-8
Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-9
; Sequence 9, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-10
; Sequence 10, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-10
Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-11
; Sequence 11, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-11
Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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US-09-687-156A-7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-7
Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-8
; Sequence 8, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-8
Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-11
; Sequence 11, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-262N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-11
Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
Db 1 GPRP 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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Db 1 GPRP 4

RESULT 50

US-09-687-156A-12
; Sequence 12, Application US/09687156A
; GENERAL INFORMATION:
; APPLICANT: Thaler, David S
; APPLICANT: Messner, Bradley T
; TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
; TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
; FILE REFERENCE: 600-1-282N
; CURRENT APPLICATION NUMBER: US/09/687,156A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-12

Query Match 100.0%; Score 25; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

||||

Db 1 GPRP 4

Search completed: September 7, 2004, 19:09:11
Job time : 418 secs

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OM protein - protein search, using sw model

Run on: September 7, 2004, 19:58:53 ; Search time 60 Seconds
(without alignments)

8.622 Million cell updates/sec

Title: US-09-931-009A-2

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table:

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Searched: 702585 seqs, 129335945 residues

Total number of hits satisfying chosen parameters: 702585

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

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1: /cgn2_6/ptodata/2/paa/pct NEW COMB.pcp.*
2: /cgn2_6/ptodata/2/paa/US06 NEW COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07 NEW COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US08 NEW COMB.pcp.*
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6: /cgn2_6/ptodata/2/paa/US10 NEW COMB.pcp.*
7: /cgn2_6/ptodata/2/paa/US60 NEW COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	4	1	PCT-US04-10121-1
2	25	100.0	4	1	PCT-US04-16828-4
3	25	100.0	4	1	PCT-US03-40762-1
4	25	100.0	6	1	PCT-BR03-00192A-109
5	25	100.0	6	1	PCT-BR03-00192A-110
6	25	100.0	6	1	PCT-BR03-00192A-111
7	25	100.0	7	1	PCT-BR03-00192A-246
8	25	100.0	7	1	PCT-BR03-00192A-247
9	25	100.0	7	1	PCT-BR03-00192A-248
10	25	100.0	7	6	US-10-459-030B-60
11	25	100.0	7	6	US-10-459-030B-64
12	25	100.0	8	6	US-10-459-030B-68
13	25	100.0	8	6	US-10-459-030B-72
14	25	100.0	9	6	US-10-459-030B-76
15	25	100.0	9	6	US-10-459-030B-80
16	25	100.0	10	6	US-10-459-030B-84
17	25	100.0	10	6	US-10-459-030B-88
18	25	100.0	11	1	PCT-BR03-00192A-527
19	25	100.0	11	1	PCT-BR03-00192A-534
20	25	100.0	11	1	PCT-BR03-00192A-540
21	25	100.0	11	1	PCT-BR03-00192A-546
22	25	100.0	11	6	US-10-459-030B-92
23	25	100.0	11	6	US-10-459-030B-96
24	25	100.0	12	6	US-10-459-030B-100
25	25	100.0	12	6	US-10-459-030B-104
26	25	100.0	13	6	US-10-459-030B-108

27	25	100.0	13	6	US-10-459-030B-112	Sequence 112, App
28	25	100.0	14	6	US-10-782-269-6	Sequence 6, Appli
29	25	100.0	14	6	US-10-782-269-7	Sequence 7, Appli
30	25	100.0	14	6	US-10-459-030B-116	Sequence 116, App
31	25	100.0	14	6	US-10-459-030B-120	Sequence 120, App
32	25	100.0	15	6	US-10-487-886-11	Sequence 11, Appl
33	25	100.0	15	6	US-10-459-030B-124	Sequence 124, App
34	25	100.0	15	6	US-10-459-030B-128	Sequence 128, App
35	25	100.0	16	6	US-10-459-030B-132	Sequence 132, App
36	25	100.0	16	6	US-10-459-030B-136	Sequence 136, App
37	25	100.0	17	6	US-10-459-030B-140	Sequence 140, App
38	25	100.0	17	6	US-10-459-030B-144	Sequence 144, App
39	25	100.0	18	6	US-10-459-030B-148	Sequence 148, App
40	25	100.0	18	6	US-10-459-030B-152	Sequence 152, App
41	25	100.0	18	6	US-10-897-406-37	Sequence 37, Appl
42	25	100.0	18	6	US-10-897-406-38	Sequence 38, Appl
43	25	100.0	18	6	US-10-729-441-37	Sequence 37, Appl
44	25	100.0	18	6	US-10-729-441-38	Sequence 38, Appl
45	25	100.0	19	6	US-10-459-030B-156	Sequence 156, App
46	25	100.0	19	6	US-10-459-030B-160	Sequence 160, App
47	25	100.0	20	6	US-10-459-030B-164	Sequence 164, App
48	25	100.0	20	6	US-10-459-030B-168	Sequence 168, App
49	25	100.0	20	6	US-10-776-013-598	Sequence 598, App
50	25	100.0	21	5	US-09-833-245A-551	Sequence 551, App
51	25	100.0	21	6	US-10-100-683-9638	Sequence 9638, Ap
52	25	100.0	21	6	US-10-459-030B-172	Sequence 172, App
53	25	100.0	21	6	US-10-459-030B-176	Sequence 176, App
54	25	100.0	22	6	US-10-459-030B-180	Sequence 180, App
55	25	100.0	22	6	US-10-459-030B-184	Sequence 184, App
56	25	100.0	23	6	US-10-459-030B-188	Sequence 188, App
57	25	100.0	23	6	US-10-459-030B-192	Sequence 192, App
58	25	100.0	24	5	US-09-952-432C-5	Sequence 5, Appli
59	25	100.0	24	6	US-10-459-030B-196	Sequence 196, App
60	25	100.0	24	6	US-10-459-030B-200	Sequence 200, App
61	25	100.0	24	6	US-10-660-811A-246	Sequence 246, App
62	25	100.0	24	6	US-10-660-811A-249	Sequence 249, App
63	25	100.0	25	6	US-10-459-030B-204	Sequence 204, App
64	25	100.0	25	6	US-10-459-030B-208	Sequence 208, App
65	25	100.0	25	6	US-10-868-184A-3218	Sequence 3218, Ap

ALIGNMENTS

RESULT 1

PCT-US04-10121-1
; Sequence 1, Application PC/TUS0410121
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN INC.
; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; TITLE OF INVENTION: METHODS FOR NEURAL DIFFERENTIATION OF EMBRYONIC STEM
; TITLE OF INVENTION: CELLS USING PROTEASE PASSAGING TECHNIQUES
; FILE REFERENCE: 18377-0031
; CURRENT APPLICATION NUMBER: PCT/US04/10121
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,090
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
PCT-US04-10121-1

Query Match 100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4

```

Db      1 GPRP 4
|||||
RESULT 2
PCT-US04-16828-4
; Sequence 4, Application PC/TUS0416828
; GENERAL INFORMATION:
; APPLICANT: University of Texas
; TITLE OF INVENTION: Micropositioning Cells for Tissue
; TITLE OF INVENTION: Engineering
; FILE REFERENCE: 21105.0003P1
; CURRENT APPLICATION NUMBER: PCT/US04/16828
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: 60/474,574
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: synthetic construct
PCT-US04-16828-4

Query Match      100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
|||||
Db      1 GPRP 4

RESULT 3
PCT-US03-40762-1
; Sequence 1, Application PC/TUS0340762
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL CELL PRODUCTION AND
; TITLE OF INVENTION: STABILIZATION
; FILE REFERENCE: 18377-0028
; CURRENT APPLICATION NUMBER: PCT/US03/40762
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: 60/434,786
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US03-40762-1

Query Match      100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
|||||
Db      1 GPRP 4

RESULT 4
PCT-BR03-00192A-109
; Sequence 109, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et al
; TITLE OF INVENTION: Pharmacological Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particularly Of Bothrops jarar
; TITLE OF INVENTION: Vasopecticases Inhibitors, Evasins, Their Analogs, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxylic acid
PCT-BR03-00192A-109

Query Match      100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
|||||
Db      3 GPRP 6

RESULT 5
PCT-BR03-00192A-110
; Sequence 110, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et al
; TITLE OF INVENTION: Pharmacological Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particularly Of Bothrops jarar
; TITLE OF INVENTION: Vasopecticases Inhibitors, Evasins, Their Analogs, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 110
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxylic acid
PCT-BR03-00192A-110

Query Match      100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
|||||
Db      3 GPRP 6

RESULT 6
PCT-BR03-00192A-111
; Sequence 111, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et al
; TITLE OF INVENTION: Pharmacological Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particularly Of Bothrops jarar
; TITLE OF INVENTION: Vasopecticases Inhibitors, Evasins, Their Analogs, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 110
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxylic acid
PCT-BR03-00192A-111

Query Match      100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GPRP 4
|||||
Db      3 GPRP 6

```

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; TITLE OF INVENTION: Vasopectidases Inhibitors, Evasins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 111
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
PCT-BR03-00192A-111

Query Match      100.0%; Score 25; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 3 GPRP 6

RESULT 7
PCT-BR03-00192A-245
; Sequence 246, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
; TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particular Of Bothrops jara
; TITLE OF INVENTION: Vasopectidases Inhibitors, Evasins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 246
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
PCT-BR03-00192A-246

Query Match      100.0%; Score 25; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 3 GPRP 6

RESULT 8
PCT-BR03-00192A-247
; Sequence 247, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
; TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particular Of Bothrops jara
; TITLE OF INVENTION: Vasopectidases Inhibitors, Evasins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
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; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 247
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
PCT-BR03-00192A-247

Query Match      100.0%; Score 25; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 3 GPRP 6

RESULT 9
PCT-BR03-00192A-248
; Sequence 248, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
; TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particular Of Bothrops jara
; TITLE OF INVENTION: Vasopectidases Inhibitors, Evasins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 248
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
PCT-BR03-00192A-248

Query Match      100.0%; Score 25; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 3 GPRP 6

RESULT 10
US-10-459-030B-60
; Sequence 60, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
```

; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(7)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-60

Query Match 100.0%; Score 25; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 11
US-10-459-030B-64
; Sequence 64, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(7)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-64

Query Match 100.0%; Score 25; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 12
US-10-459-030B-68
; Sequence 68, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
US-10-459-030B-68

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(8)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-68

Query Match 100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 13
US-10-459-030B-72
; Sequence 72, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(8)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-72

Query Match 100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 14
US-10-459-030B-76
; Sequence 76, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
US-10-459-030B-76

; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(9)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-76

Query Match 100.0%; Score 25; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 15
US-10-459-030B-80
; Sequence 80, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(9)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-80

Query Match 100.0%; Score 25; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 16
US-10-459-030B-84
; Sequence 84, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(10)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-84

Query Match 100.0%; Score 25; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 17
US-10-459-030B-88
; Sequence 88, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(10)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-88

Query Match 100.0%; Score 25; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 1 GPRP 4

RESULT 18
PCT-BR03-00192A-527
; Sequence 527, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Pharmaceutica Ltda.; et al
; TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
; FILE REFERENCE: Secreted by The Snake Venom Glands, Particular Of Bothrops jara
; TITLE OF INVENTION: Vasoepitidases Inhibitors, Evamins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof, For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 527

```
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxylic acid
PCT-BR03-00192A-540

Query Match      100.0%; Score 25; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 2 GPRP 5

RESULT 19
PCT-BR03-00192A-534
; Sequence 534, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
; TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particularly Of Bothrops jara
; TITLE OF INVENTION: Vasopectidases Inhibitors, Evasins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 534
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxylic acid
PCT-BR03-00192A-534

Query Match      100.0%; Score 25; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 2 GPRP 5

RESULT 20
PCT-BR03-00192A-540
; Sequence 540, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
; TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particularly Of Bothrops jara
; TITLE OF INVENTION: Vasopectidases Inhibitors, Evasins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 540
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxylic acid
PCT-BR03-00192A-540

Query Match      100.0%; Score 25; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 2 GPRP 5

RESULT 21
PCT-BR03-00192A-546
; Sequence 546, Application PC/TBR0300192A
; GENERAL INFORMATION:
; APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
; TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
; TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particularly Of Bothrops jara
; TITLE OF INVENTION: Vasopectidases Inhibitors, Evasins, Their Analogues, Derivatives
; TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
; TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
; FILE REFERENCE: PI0205449-3
; CURRENT APPLICATION NUMBER: PCT/BR03/00192A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: BR PI0205449-3
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 594
; SEQ ID NO 546
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Bothrops jararaca
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)
; OTHER INFORMATION: Xaa is a pyrrolidone carboxylic acid
PCT-BR03-00192A-546

Query Match      100.0%; Score 25; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 2 GPRP 5

RESULT 22
US-10-459-030B-92
; Sequence 92, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/A01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
```

; LOCATION: (6)...(11)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-92

Query Match 100.0%; Score 25; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
DB 1 GPRP 4

RESULT 23
US-10-459-030B-96
; Sequence 96, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(11)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-96

Query Match 100.0%; Score 25; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
DB 1 GPRP 4

RESULT 24
US-10-459-030B-100
; Sequence 100, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(12)

; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-100

Query Match 100.0%; Score 25; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
DB 1 GPRP 4

RESULT 25
US-10-459-030B-104
; Sequence 104, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(12)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-104

Query Match 100.0%; Score 25; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
DB 1 GPRP 4

RESULT 26
US-10-459-030B-108
; Sequence 108, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(13)
; OTHER INFORMATION: Xaa=any amino acid

```
US-10-459-030B-106
Query Match      100.0%; Score 25; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 1 GPRP 4

RESULT 27
US-10-459-030B-112
; Sequence 112, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(13)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-112

Query Match      100.0%; Score 25; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 1 GPRP 4

RESULT 28
US-10-782-269-6
; Sequence 6, Application US/10782269
; GENERAL INFORMATION:
; APPLICANT: Lopez-Avila, Viorica
; APPLICANT: Hirschberg, David
; TITLE OF INVENTION: Methods and compositions for assessing a
; FILE REFERENCE: 10031188-1
; CURRENT APPLICATION NUMBER: US/10/782,269
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-782-269-6

Query Match      100.0%; Score 25; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 1 GPRP 4

US-10-459-030B-120
Query Match      100.0%; Score 25; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 1 GPRP 4

US-10-459-030B-116
Query Match      100.0%; Score 25; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 4 GPRP 7

RESULT 30
US-10-459-030B-116
; Sequence 116, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(14)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-116

Query Match      100.0%; Score 25; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
    ||||
Db 1 GPRP 4

RESULT 31
US-10-459-030B-120
; Sequence 120, Application US/10459030B
```



```
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(14)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-120
```

```
Query Match 100.0%; Score 25; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GPRP 4
Db 1 GPRP 4
```

```
RESULT 32
US-10-487-886-11
; Sequence 11, Application US/10487886
; GENERAL INFORMATION:
; APPLICANT: Barske, Carmen
; APPLICANT: Frentzel, Stefan
; APPLICANT: Kaupmann, Klemens
; APPLICANT: Sommer, Bernd Josef
; APPLICANT: Mir, Anis Khuroo
; TITLE OF INVENTION: Nogo Receptor Homologues and their use
; FILE REFERENCE: 4-32101/A
; CURRENT APPLICATION NUMBER: US/10/487,886
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 60/315110
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: for immunizing
US-10-487-886-11
```

```
Query Match 100.0%; Score 25; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GPRP 4
Db 5 GPRP 8
```

```
RESULT 33
US-10-459-030B-124
; Sequence 124, Application US/10459030B
; GENERAL INFORMATION:
```

```
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(15)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-124
```

```
Query Match 100.0%; Score 25; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GPRP 4
Db 1 GPRP 4
```

```
RESULT 34
US-10-459-030B-128
; Sequence 128, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(15)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-128
```

```
Query Match 100.0%; Score 25; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GPRP 4
Db 1 GPRP 4
```

```
RESULT 35
US-10-459-030B-132
; Sequence 132, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
```

;; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
;; FILE REFERENCE: A35859 PCT USA A 071986.0248
;; CURRENT APPLICATION NUMBER: US/10/459,030B
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/AT01/00387
;; PRIOR FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: AT 2063/2000
;; PRIOR FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 296
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 132
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: peptide of formula II
;; NAME/KEY: VARIANT
;; LOCATION: (6)...(16)
;; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-132

Query Match 100.0%; Score 25; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 36
US-10-459-030B-136
;; Sequence 136, Application US/10459030B
;; GENERAL INFORMATION:
;; APPLICANT: Petzelbauer, Peter
;; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
;; FILE REFERENCE: A35859 PCT USA A 071986.0248
;; CURRENT APPLICATION NUMBER: US/10/459,030B
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/AT01/00387
;; PRIOR FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: AT 2063/2000
;; PRIOR FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 296
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 136
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: peptide of formula II
;; NAME/KEY: VARIANT
;; LOCATION: (6)...(16)
;; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-136

Query Match 100.0%; Score 25; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 37
US-10-459-030B-140
;; Sequence 140, Application US/10459030B
;; GENERAL INFORMATION:
;; APPLICANT: Petzelbauer, Peter
;; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF

;; FILE REFERENCE: A35859 PCT USA A 071986.0248
;; CURRENT APPLICATION NUMBER: US/10/459,030B
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/AT01/00387
;; PRIOR FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: AT 2063/2000
;; PRIOR FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 296
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 140
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: peptide of formula II
;; NAME/KEY: VARIANT
;; LOCATION: (6)...(17)
;; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-140

Query Match 100.0%; Score 25; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 38
US-10-459-030B-144
;; Sequence 144, Application US/10459030B
;; GENERAL INFORMATION:
;; APPLICANT: Petzelbauer, Peter
;; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
;; FILE REFERENCE: A35859 PCT USA A 071986.0248
;; CURRENT APPLICATION NUMBER: US/10/459,030B
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: PCT/AT01/00387
;; PRIOR FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: AT 2063/2000
;; PRIOR FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 296
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 144
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: peptide of formula II
;; NAME/KEY: VARIANT
;; LOCATION: (6)...(17)
;; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-144

Query Match 100.0%; Score 25; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
Db 1 GPRP 4

RESULT 39
US-10-459-030B-148
;; Sequence 148, Application US/10459030B
;; GENERAL INFORMATION:
;; APPLICANT: Petzelbauer, Peter
;; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
;; FILE REFERENCE: A35859 PCT USA A 071986.0248

; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(18)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-148

Query Match 100.0%; Score 25; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 1 GRRP 4

RESULT 40

US-10-459-030B-152
; Sequence 152, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(18)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-152

Query Match 100.0%; Score 25; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 1 GRRP 4

RESULT 41

US-10-897-406-37
; Sequence 37, Application US/10897406
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8338
; CURRENT APPLICATION NUMBER: US/10/897,406

; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US/10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-897-406-37

Query Match 100.0%; Score 25; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 4 GRRP 7

RESULT 42

US-10-897-406-38
; Sequence 38, Application US/10897406
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8338
; CURRENT APPLICATION NUMBER: US/10/897,406
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US/10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-897-406-38

Query Match 100.0%; Score 25; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 4 GRRP 7

RESULT 43

US-10-729-441-37
; Sequence 37, Application US/10729441
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/729,441
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US/10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-729-441-37

Query Match 100.0%; Score 25; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRP 4
Db 1 GRRP 4

```
Db          4 GPRP 7

; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(19)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-160

Query Match      100.0%; Score 25; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 47
US-10-459-030B-164
; Sequence 164, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(20)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-164

Query Match      100.0%; Score 25; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
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Db      1 GPRP 4

RESULT 48
US-10-459-030B-168
; Sequence 168, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
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Db          4 GPRP 7

; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10729441
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/729,441
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-729-441-38

Query Match      100.0%; Score 25; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      4 GPRP 7

RESULT 45
US-10-459-030B-156
; Sequence 156, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; NAME/KEY: VARIANT
; LOCATION: (6)...(19)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-156

Query Match      100.0%; Score 25; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRP 4
      ||||
Db      1 GPRP 4

RESULT 46
US-10-459-030B-160
; Sequence 160, Application US/10459030B
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
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; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of formula II
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (6)...(20)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-168

Query Match 100.0%; Score 25; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
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Db 1 GPRP 4

RESULT 49

US-10-776-013-598
; Sequence 598, Application US/10776013
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 598
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-598

Query Match 100.0%; Score 25; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4

Db |||
14 GPRP 17

RESULT 50

US-09-833-245A-551
; Sequence 551, Application US/09833245A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546
; CURRENT APPLICATION NUMBER: US/09/833,245A
; CURRENT FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 2277
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 551
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245A-551

Query Match 100.0%; Score 25; DB 5; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRP 4
|||
Db 8 GPRP 11

Search completed: September 7, 2004, 19:10:18
Job time : 61 secs

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